

**Annex 1**

**PBP2X AMINO ACID SEQUENCE ACCESSION NUMBERS  
AVAILABLE IN THE SEQUENCE DATA BASES  
AT THE PRIORITY DATE (11 JULY 2002)**

1PMD  
P14677  
AAC45547  
AAC95456  
AAD45394  
AAF17263  
AAF17264  
AAF17265  
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AAF17267  
AAF17268  
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AAF17270  
AAL77081  
AAL82396  
AAL82397  
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AAL82401  
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BAA75536  
BAA75537

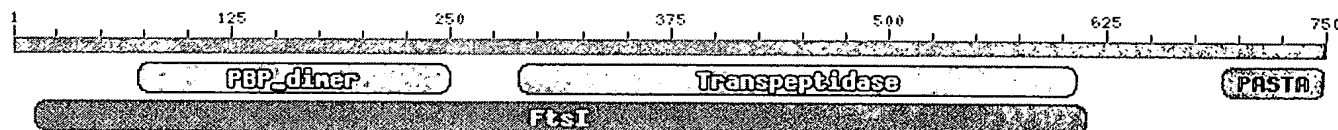
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CAA46261  
CAA46263  
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CAA46266  
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CAA67010  
CAA67011  
CAA67012  
CAA67013  
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CAA71562  
CAA71563  
CAA71564  
CAA88919  
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CAB01929  
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CAB65443  
CAB65444  
CAB65445  
CAB65446  
CAB65447  
CAB65448  
CAC20946  
CAC20947  
CAC20948  
CAC20949  
CAC20950  
CAC20951  
CAC20952  
CAC20953  
CAC20954  
CAC20955  
CAC43044  
CAC43045

**BLAST Basic Local Alignment Search Tool**

Job Title: PBP2X-R6

Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



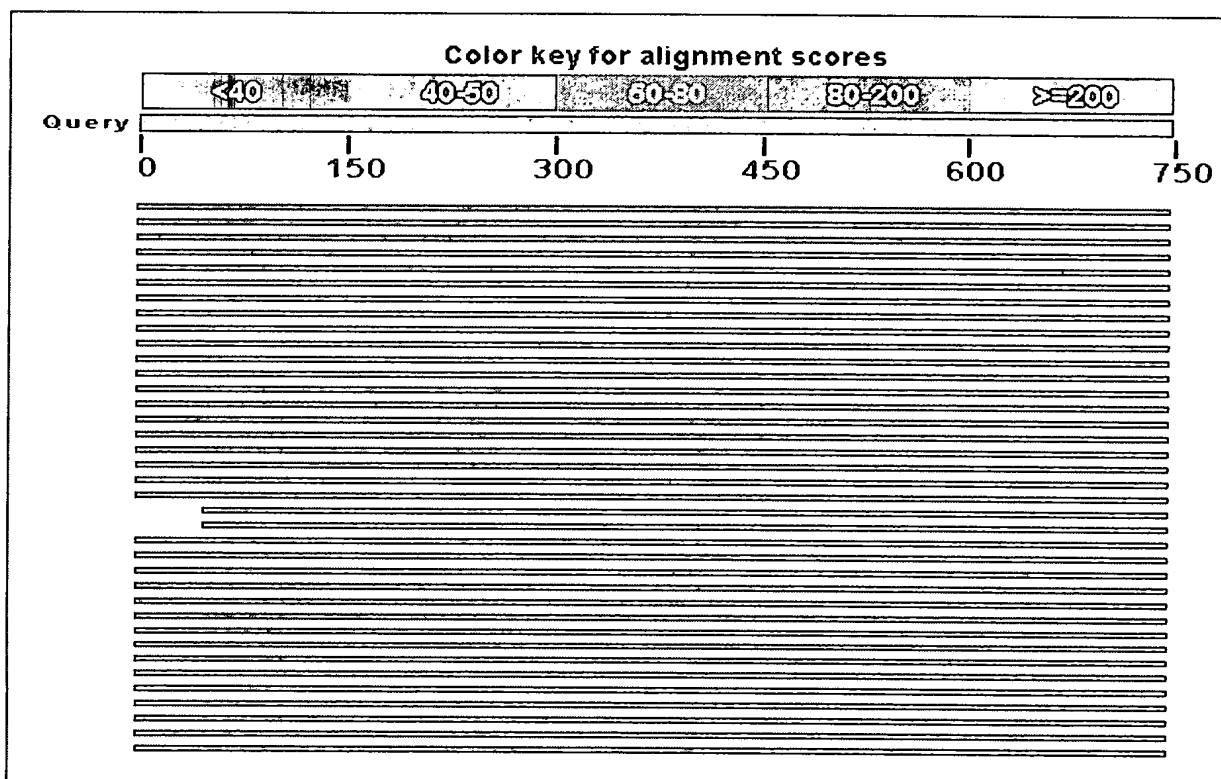
- Your search is limited to records matching entrez query: PBP2x penicillin binding protein AND Streptococcus pneumoniae [ORGN].

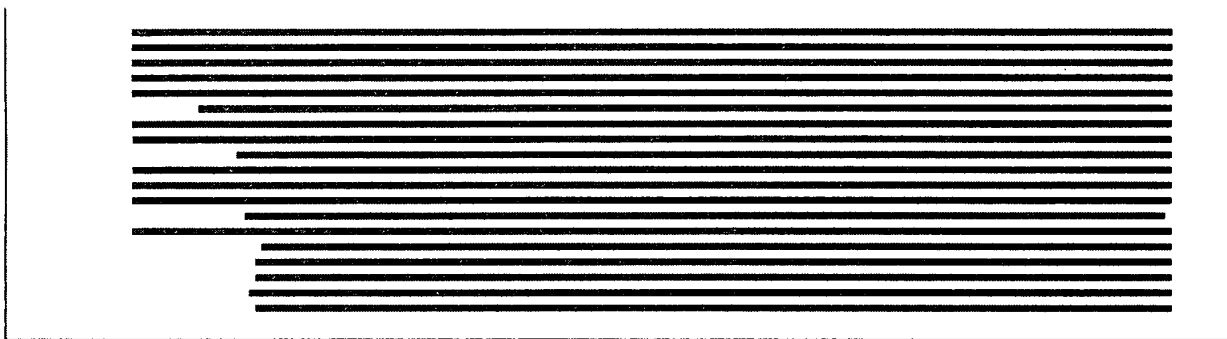
**BLASTP 2.2.16 (Mar-25-2007)**

**Reference:** Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

**Reference:** Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005. RID: 5ZZGCTZA015 **Database:** All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects 4,990,428 sequences; 1,725,524,515 total letters

Query= Length=750

**Distribution of 100 Blast Hits on the Query Sequence**




Distance tree of results <sup>NEW</sup> Related Structures

Sequences producing significant alignments:

	Score (Bits)	E Value	
sp P59676 PBPX_STRR6 Penicillin-binding protein 2X (PBP-2X) (PBP	1441	0.0	<b>G</b>
dbj BAD00902.1  penicillin-binding protein 2X [Streptococcus pne	1439	0.0	
dbj BAD67448.1  penicillin-binding protein 2X [Streptococcus pne	1438	0.0	
sp P14677 PBPX_STRPN Penicillin-binding protein 2x (PBP-2x) (PBP	1438	0.0	
dbj BAD00901.1  penicillin-binding protein 2X [Streptococcus pne	1438	0.0	
dbj BAD00904.1  penicillin-binding protein 2X [Streptococcus pne	1436	0.0	
gb AAF17263.1 AF210753_1 penicillin-binding protein 2X [Streptoc	1434	0.0	
dbj BAD00905.1  penicillin-binding protein 2X [Streptococcus ...	1418	0.0	
dbj BAD00912.1  penicillin-binding protein 2X [Streptococcus pne	1415	0.0	
gb AAF17266.1 AF210756_1 penicillin-binding protein 2X [Streptoc	1397	0.0	
gb AAF17265.1 AF210755_1 penicillin-binding protein 2X [Strep...	1395	0.0	
dbj BAD00920.1  penicillin-binding protein 2X [Streptococcus pne	1368	0.0	
dbj BAD00903.1  penicillin-binding protein 2X [Streptococcus pne	1367	0.0	
dbj BAD00916.1  penicillin-binding protein 2X [Streptococcus pne	1365	0.0	
gb AAF17267.1 AF210757_1 penicillin-binding protein 2X [Streptoc	1361	0.0	
dbj BAD00919.1  penicillin-binding protein 2X [Streptococcus pne	1357	0.0	
gb AAF17264.1 AF210754_1 penicillin-binding protein 2X [Streptoc	1349	0.0	
dbj BAD00929.1  penicillin-binding protein 2X [Streptococcus pne	1348	0.0	
dbj BAD00909.1  penicillin-binding protein 2X [Streptococcus pne	1345	0.0	
dbj BAD00907.1  penicillin-binding protein 2X [Streptococcus pne	1344	0.0	
pdb 1QME A Chain A, Penicillin-Binding Protein 2x (Pbp-2x) >p...	1344	0.0	<b>S</b>
pdb 1PYY A Chain A, Double Mutant Pbp2x T338aM339F FROM STREP...	1341	0.0	<b>S</b>
dbj BAD00918.1  penicillin-binding protein 2X [Streptococcus pne	1340	0.0	
dbj BAD00910.1  penicillin-binding protein 2X [Streptococcus pne	1336	0.0	
dbj BAD00923.1  penicillin-binding protein 2X [Streptococcus ...	1327	0.0	
dbj BAD00917.1  penicillin-binding protein 2X [Streptococcus pne	1324	0.0	
dbj BAD00927.1  penicillin-binding protein 2X [Streptococcus pne	1323	0.0	
dbj BAD00913.1  penicillin-binding protein 2X [Streptococcus pne	1318	0.0	
dbj BAD00938.1  penicillin-binding protein 2X [Streptococcus pne	1316	0.0	
dbj BAD00922.1  penicillin-binding protein 2X [Streptococcus pne	1316	0.0	
dbj BAD00925.1  penicillin-binding protein 2X [Streptococcus pne	1315	0.0	
dbj BAD00926.1  penicillin-binding protein 2X [Streptococcus pne	1315	0.0	
gb AAF17268.1 AF210758_1 penicillin-binding protein 2X [Streptoc	1313	0.0	
gb AAF17270.1 AF210760_1 penicillin-binding protein 2X [Streptoc	1312	0.0	
dbj BAD00932.1  penicillin-binding protein 2X [Streptococcus pne	1312	0.0	
gb AAF17269.1 AF210759_1 penicillin-binding protein 2X [Streptoc	1312	0.0	
dbj BAD00936.1  penicillin-binding protein 2X [Streptococcus pne	1312	0.0	
gb AAL77081.1 AF468152_1 penicillin-binding protein 2X [Streptoc	1307	0.0	
dbj BAD00939.1  penicillin-binding protein 2X [Streptococcus pne	1307	0.0	
dbj BAD00935.1  penicillin-binding protein 2X [Streptococcus pne	1306	0.0	
dbj BAD00906.1  penicillin-binding protein 2X [Streptococcus pne	1305	0.0	
dbj BAD00937.1  penicillin-binding protein 2X [Streptococcus pne	1303	0.0	
pdb 1RP5 A Chain A, Pbp2x From Streptococcus Pneumoniae Strai...	1297	0.0	<b>S</b>
dbj BAD00914.1  penicillin-binding protein 2X [Streptococcus ...	1296	0.0	
dbj BAD00928.1  penicillin-binding protein 2X [Streptococcus pne	1294	0.0	
pdb 1PMD  Chain , Penicillin-Binding Protein 2x (Pbp-2x)	1294	0.0	<b>S</b>
gb AAC45547.1  low-affinity penicillin-binding protein 2X [St...	1284	0.0	
dbj BAD00915.1  penicillin-binding protein 2X [Streptococcus pne	1279	0.0	
dbj BAD00940.1  penicillin-binding protein 2X [Streptococcus pne	1275	0.0	
gb AAY56845.1  penicillin-binding protein 2X [Streptococcus pneu	1271	0.0	
dbj BAD00908.1  penicillin-binding protein 2X [Streptococcus ...	1269	0.0	
gb ABB46504.1  penicillin binding protein 2x [Streptococcus p...	1258	0.0	
gb AAN32862.1  penicillin-binding protein 2X [Streptococcus pneu	1235	0.0	
gb AAN32857.1  penicillin-binding protein 2X [Streptococcus p...	1234	0.0	
emb CAB65447.1  penicillin binding protein 2x [Streptococcus pne	1230	0.0	
gb AAN32865.1  penicillin-binding protein 2X [Streptococcus pneu	1222	0.0	
emb CAD90770.1  penicillin-binding protein 2x [Streptococcus pne	1217	0.0	
emb CAD90771.2  penicillin-binding protein 2x [Streptococcus pne	1209	0.0	
gb AAY56843.1  penicillin-binding protein 2X [Streptococcus p...	1207	0.0	
gb AAY56850.1  penicillin-binding protein 2X [Streptococcus pneu	1206	0.0	
gb AAY56847.1  penicillin-binding protein 2X [Streptococcus pneu	1204	0.0	

gb AA56846.1	penicillin-binding protein 2X [Streptococcus pneu	1198	0.0
gb AA56857.1	penicillin-binding protein 2X [Streptococcus pneu	1197	0.0
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gb AAN32852.1	penicillin-binding protein 2X [Streptococcus p...	1187	0.0
gb AAN32861.1	penicillin-binding protein 2X [Streptococcus pneu	1186	0.0
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pdb 1K25 A	Chain A, Pbp2x From A Highly Penicillin-Resistant ...	1183	0.0
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gb ABB46506.1	penicillin binding protein 2x [Streptococcus pneu	1181	0.0
gb AA56848.1	penicillin-binding protein 2X [Streptococcus pneu	1180	0.0
emb CAB65446.1	penicillin binding protein 2x [Streptococcus pne	1179	0.0
gb AAN32859.1	penicillin-binding protein 2X [Streptococcus pneu	1176	0.0
gb AA56854.1	penicillin-binding protein 2X [Streptococcus pneu	1174	0.0
gb AAN32860.1	penicillin-binding protein 2X [Streptococcus pneu	1174	0.0
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emb CAB65445.1	penicillin binding protein 2x [Streptococcus pne	1170	0.0
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gb AA56838.1	penicillin-binding protein 2X [Streptococcus pneu	1165	0.0
emb CAB65442.1	penicillin binding protein 2x [Streptococcus pne	1165	0.0
emb CAB65443.1	penicillin binding protein 2x [Streptococcus pne	1162	0.0
gb AA56842.1	penicillin-binding protein 2X [Streptococcus pneu	1160	0.0
gb AA56852.1	penicillin-binding protein 2X [Streptococcus pneu	1158	0.0
emb CAB65441.1	penicillin binding protein 2x [Streptococcus pne	1157	0.0
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gb AA56849.1	penicillin-binding protein 2X [Streptococcus pneu	1155	0.0
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emb CAA88919.1	penicillin-binding protein 2x [Streptococcus pne	1149	0.0
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emb CAA67012.1	penicillin-binding protein [Streptococcus pneumo	1148	0.0
emb CAA67010.1	penicillin-binding protein [Streptococcus pneumo	1146	0.0
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gb AAN32864.1	penicillin-binding protein 2X [Streptococcus pneu	1143	0.0
emb CAA67011.1	penicillin-binding protein [Streptococcus pneumo	1141	0.0
gb AA56840.1	penicillin-binding protein 2X [Streptococcus pneu	1140	0.0
gb AAN32856.1	penicillin-binding protein 2X [Streptococcus pneu	1139	0.0
gb ABB46508.1	penicillin binding protein 2x [Streptococcus pneu	1135	0.0
gb AA56855.1	penicillin-binding protein 2X [Streptococcus pneu	1135	0.0

## Alignments

>sp|P59676|PBPX\_STRR6  Penicillin-binding protein 2X (PBP-2X) (PBP2X)  
Length=750

Score = 1441 bits (3729), Expect = 0.0, Method: Composition-based stats.  
Identities = 750/750 (100%), Positives = 750/750 (100%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYPGSTMKVMMLAAAI DNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYPGSTMKVMMLAAAI DNNTFPGGEVFN	360

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Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420

Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL 600
Sbjct 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL 600

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLIILSDKAEVDPMYGWTKETATLAKWLNIELEF 720
Sbjct 661 IVVGTGTKIKNSSAEEGKNLAPNQVLIILSDKAEVDPMYGWTKETATLAKWLNIELEF 720

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

```

>dbj|BAD00902.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1439 bits (3726), Expect = 0.0, Method: Composition-based stats.  
Identities = 749/750 (99%), Positives = 749/750 (99%), Gaps = 0/750 (0%)

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Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFVFAIFLVNFAVVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFVFAIFLVNFAVVIIGTGTRFGTDLAK 60

Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR 240

Query 241 LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300

Query 301 ILATTQRPFTFADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFN 360
Sbjct 301 ILATTQRPFTFADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFN 360

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420

Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL 600
Sbjct 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL 600

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLIILSDKAEVDPMYGWTKETATLAKWLNIELEF 720
Sbjct 661 IVVGTGTKIKNSSAEEGKNLAPNQVLIILSDKAEVDPMYGWTKETATLAKWLNIELEF 720

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

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Sbjct 721 QGSGSTVQKQDV RANTAIKDIKKITLTLGD 750

>dbj|BAD67448.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1438 bits (3723), Expect = 0.0, Method: Composition-based stats.  
Identities = 748/750 (99%), Positives = 748/750 (99%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGVEFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGVEFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIKNSSAEEGKNLAPNQVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF	720
Query	721	QGSGSTVQKQDV RANTAIKDIKKITLTLGD 750	
Sbjct	721	QGSGSTVQKQDV RANTAIKDIKKITLTLGD 750	

>sp|P14677|PBPX\_STRPN Penicillin-binding protein 2x (PBP-2x) (PBP2x)  
Length=750

Score = 1438 bits (3723), Expect = 0.0, Method: Composition-based stats.  
Identities = 749/750 (99%), Positives = 749/750 (99%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300



Sbjct	241	LGNIIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLILSDKAEVDPMYGWTKETATLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIKNSSAEEGKNLAPNQVLILSDKAEVDPMYGWTKETATLAKWLNIELEF	720
Query	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD	750
Sbjct	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD	750

>dbj|BAD00901.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1438 bits (3722), Expect = 0.0, Method: Composition-based stats.  
Identities = 748/750 (99%), Positives = 749/750 (99%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLQVVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLQVVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLILSDKAEVDPMYGWTKETATLAKWLNIELEF	720

```

_Sbjct 661  IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDK EEVDPMYGWTKETAEATLAKWLNIELEF 720
            IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKVEEVDPMYGWTKETAEATLAKWLNIELEF
Query 721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
            QGSGSTVQKQDVRANTAIKDIKKITLTLGD
_Sbjct 721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
            QGSGSTVQKQDVRANTAIKDIKKITLTLGD

```

>dbj|BAD00904.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1436 bits (3718), Expect = 0.0, Method: Composition-based stats.  
Identities = 748/750 (99%), Positives = 749/750 (99%), Gaps = 0/750 (0%)

```

Query 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180

Query 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240

Query 241    LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE 300
Sbjct 241    LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE 300

Query 301    ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFN 360
Sbjct 301    ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFN 360

Query 361    SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGGDATWLDYLNRFK 420
Sbjct 361    SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGGDATWLDYLNRFK 420

Query 421    FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421    FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480

Query 481    SAIYDPNDQTARKSQKEIVGNPVSFDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481    SAIYDPNDQTARKSQKEIVGNPVSFDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540

Query 541    GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541    GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600

Query 601    GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601    EEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660

Query 661    IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWTKETAEATLAKWLNIELEF 720
Sbjct 661    IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWTKETAEATLAKWLNIELEF 720

Query 721    QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721    QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

```

>gb|AAF17263.1|AF210753\_1 penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1434 bits (3713), Expect = 0.0, Method: Composition-based stats.  
Identities = 747/750 (99%), Positives = 748/750 (99%), Gaps = 0/750 (0%)

```

Query 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180

Query 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240

```

Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFPGGVEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFPGGVEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWTKETATLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWTKETATLAKWLNIELEF	720
Query	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD	750
Sbjct	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD	750

>dbj|BAD00905.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
 dbj|BAD00921.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
 Length=750

Score = 1418 bits (3670), Expect = 0.0, Method: Composition-based stats.  
 Identities = 737/750 (98%), Positives = 745/750 (99%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLQVVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLQVVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFPGGVEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFPGGVEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SALYDPNDQSVRKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600

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Query 601  GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601  GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660

Query 661  IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF 720
Sbjct 661  IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF 720

Query 721  QGSGSTVQKQDV RANTAIKDIKKITLTLGD 750
Sbjct 721  QGSGSTVQKQDV RANTAIKDIKKITLTLGD 750

```

>dbj|BAD00912.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1415 bits (3662), Expect = 0.0, Method: Composition-based stats.  
Identities = 734/750 (97%), Positives = 744/750 (99%), Gaps = 0/750 (0%)

```

Query 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KGNGITYANMMSIKKELEAEVKGIDF 180

Query 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSMESSLNSILAGTDGIITYEKDR 240
Sbjct 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSMESSLNILAGTDGIITYEKDR 240

Query 241    LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMATLVS AKTGE 300
Sbjct 241    LGNIVPGTEQVSQQTVDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMATLVS AKTGE 300

Query 301    ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFN 360
Sbjct 301    ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSPMKVMMLAAAI DNNTFPGGEVFN 360

Query 361    SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361    SSELKIADTIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420

Query 421    FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421    FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480

Query 481    SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481    SAIYDPNDQTARKSQKEIVGNPVSKDAAS TRT+MVLVGTDPVYGTMYNHSTGKPTVTVP 540

Query 541    GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541    GQNVALKSGTAQIADEKNGGYL+G T++IFSAVSM+PAENPDFILYVTVQQPEHYSGIQL 600

Query 601    GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601    GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660

Query 661    IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF 720
Sbjct 661    IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF 720

Query 721    QGSGSTVQKQDV RANTAIKDIKKITLTLGD 750
Sbjct 721    QGSGSTVQKQDV RANTAIKDIKKITLTLGD 750

```

>gb|AAF17266.1|AF210756\_1 penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1397 bits (3617), Expect = 0.0, Method: Composition-based stats.  
Identities = 725/750 (96%), Positives = 737/750 (98%), Gaps = 0/750 (0%)

```

Query 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

```

Query	121	KVAEVFHXYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHXYLDMEESYV EQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMATLVS AKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMATLVS AKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFP GG EVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFP GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIA S+FGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNM+LVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL	600
Sbjct	541	GQNVALKSGTA+IADEKNGGYLVG T+ IFS V+M+PAENPDFILYVTVQQPEHYSIGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFTNPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWT KETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWT K TAET AKWLNIELEF	720
Query	721	QGS GSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	

>gb|AAAF17265.1|AF210755 1 penicillin-binding protein 2X [Streptococcus pneumoniae]  
 gb|AAC95456.1| penicillin-binding protein 2x [Streptococcus pneumoniae]  
 Length=750

Score = 1395 bits (3612), Expect = 0.0, Method: Composition-based stats.  
 Identities = 723/750 (96%), Positives = 737/750 (98%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHXYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHXYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMATLVS AKTGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMATLVS AKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFP GG EVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFP GG EVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIA S+FGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540

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_Sbjct  481  SA+YDPNDQ+ RKSQKEIVGNPVSK+AAS+TR +MV+VGTD P YGTMYNHSTGK TV VP
          SALYDPNDQSVRKSQKEIVGNPVSKAASVTRDHMMVVGTDPTYGTMYNHSTGKATVNV P 540
Query    541  GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
          GQNVALKSGTA+IADEKNGGYL G T+ IFS VSM PAENPDFILYVTVQQPEHYSGIQL
_Sbjct  541  GQNVALKSGTAQIADEKNGGYLTGSTNNIFSVVSMHPAENPDFILYVTVQQPEHYSGIQL 600
Query    601  GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
          GEFANPILERASAMK+SLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP
Sbjct    601  GEFANPILERASAMKESLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Query    661  IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPDYGWTKETAETLAKWLNIELEF 720
          IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPDYGWTKETAET AKWLNIELEF
Sbjct    661  IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPDYGWTKETAETFAKWLNIELEF 720
Query    721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
          +GSGSTVQKQDVRANTAIKDIKKITLTLGD
Sbjct    721  EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

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>dbj|BAD00920.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1368 bits (3540), Expect = 0.0, Method: Composition-based stats.  
Identities = 708/750 (94%), Positives = 731/750 (97%), Gaps = 0/750 (0%)

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Query    1    MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
          MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK
Sbjct    1    MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAVFLVNFAVIIGTGTRFGTDLAK 60
Query    61    EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
          EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN
Sbjct    61    EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Query    121   KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
          KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KGNGITYANMMSIKKELE AEVKGIDF
Sbjct    121   KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGSKGNGITYANMMSIKKELETAEVKGIDF 180
Query    181   TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
          TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR
Sbjct    181   TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Query    241   LGNIVPGTEQVSQRTMDGKDVYTTISSPLOSFMETQMDAFQEKVKGKYMTATLVSAKTGE 300
          LGNIVPGTEQVSQ+T+DGKDVYTTISS LQSFMETQ+AFQEKVKGKYMTATLVSAKTGE
Sbjct    241   LGNIVPGTEQVSQQTVDGKDVYTTISSTLQSFMETQMNAFQEKVKGKYMTATLVSAKTGE 300
Query    301   ILATTQRPFTFADTKEGITEDFVWRDILYQSNEYEPGSTMKVMMMLAAIDNNTFPGGVEFN 360
          ILATTQRPFTFADTKEG+T+DFVWRDILYQSNEYEPGSTMKVM LAA+IDNNTFPGGE FN
Sbjct    301   ILATTQRPFTFADTKEGLTKEDFVWRDILYQSNEYEPGSTMKVMTLAASIDNNTFPGGVEFN 360
Query    361   SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
          SSELKIAD TIRDWDVN+GLT GRMMTF QGFA SSNVGM+LLEQKMGDATWLDYLNRFK
Sbjct    361   SSELKIADVTIRDWDVNDGLTTGRMMTFLQGFALSSNVGMSLLEQKMGDATWLDYLNRFK 420
Query    421   FGVPTREFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
          FGVPTREFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI
Sbjct    421   FGVPTREFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480
Query    481   SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDVPYGTMYNHSTGKPTVTV P 540
          SAIYD N+Q+ RKSQKEIVG PVS+DAASLRTNM+LVGTD P+YGTMYNH TGKP +TV P
Sbjct    481   SAIYDTNNQSVRKSQKEIVGKPVSEDAASLRTNMILVGTDPLYGTMYNHQTGKPIITVP 540
Query    541   GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
          GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYS QL
Sbjct    541   GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNP AENPDFILYVTVQQPEHYSAAQL 600
Query    601   GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
          GEF+NPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP
Sbjct    601   GEFNPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Query    661   IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPDYGWTKETAETLAKWLNIELEF 720
          IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPDYGWTK TAET AKWLNIELEF
Sbjct    661   IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPDYGWTKATAETFAKWLNIELEF 720
Query    721   QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
          +GSGSTVQKQDVRANTAIKDIKKITLTLGD
Sbjct    721   EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

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>dbj|BAD00903.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1367 bits (3538), Expect = 0.0, Method: Composition-based stats.  
Identities = 705/750 (94%), Positives = 727/750 (96%), Gaps = 0/750 (0%)

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Query    1    MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

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Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVN+GLT G MMTFSQGFAHSSNVGM+LLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYTGQLPADNIVNIAMSAFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKS+KEIVG PVS+DAASLRTNM+LVGTDP+YGTMYNH TGKP +TVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERA AMKDSLNLQ+TAK L+QV+ QS Y MPS+KDISPGDLAE LRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK SS EEG NL PNQQVLILSDKAEVDPMYGWTK TAET AKWLN I+LEF	720
Query	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	

>dbj|BAD00916.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1365 bits (3534), Expect = 0.0, Method: Composition-based stats.  
Identities = 706/750 (94%), Positives = 729/750 (97%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEG+T+DFVWRDILYQSNYEPGSTMKVM LA++IDNNTFP GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIAD TIRDWDVN+GLT GRMMTF QGFA SSVNGM+LLEQKMGD TWLDYLNRFK	420



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Query   421   FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI  480
Sbjct   421   FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI  480

Query   481   SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP  540
Sbjct   481   SAIYD N+Q+ RKSQKEIVG PVS+DAASLTRTNM+LVGTDP+YGTMYNH TGKP +TVP  540
        SAIYDTNNQSVRKSQKEIVGKPVSEDAASLTRTNMILVGTDPYGTMYNHYTGPPIITVP

Query   541   GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL  600
Sbjct   541   GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL  600
        GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPANPDFILYVTVQQPEHYSGIQL

Query   601   GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP  660
Sbjct   601   GEFANPILERASAMK+SLNLQ+ AK L+QV+ +S Y MPS+KDISPGDLAEELRRNLVQP  660
        GEFANPILERASAMKESLNLQSPAKNLDQVTTESYAMPSIKDISPGDLAEELRRNLVQP

Query   661   IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVPMYGTWKETAETLAKWLNIELEF  720
Sbjct   661   IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDK EEVPMYGTWKETAETLAKWLNIELEF  720
        IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKVEEVPDMPYGTWKETAETLAKWLNIELEF

Query   721   QGSGSTVQKQDVRANTAIKDIKKITLTLGD  750
Sbjct   721   QGSGSTVQKQDVRANTAIKDIKKITLTLGD  750

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>gb|AA17267.1|AF210757\_1 penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1361 bits (3522), Expect = 0.0, Method: Composition-based stats.  
Identities = 705/750 (94%), Positives = 726/750 (96%), Gaps = 0/750 (0%)

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Query   1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK  60
Sbjct   1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK  60
        MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAVFLVNFAVIIGTGTRFGTDLAK

Query   61     EAKKVHQTTTRTPAKRGTIYDRNGVPVIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN  120
Sbjct   61     EAKKVHQTTTR VPAKRGTIYDRNGVPVIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN  120
        EAKKVHQTTTRIVPAKRGTIYDRNGVPVIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN

Query   121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGGITYANMMSIKKELEAAEVKGIDF  180
Sbjct   121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGGITYANMMSIKKELE AEVKGIDF  180
        KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGGITYANMMSIKKELETAEVKGIDF

Query   181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR  240
Sbjct   181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR  240
        TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR

Query   241    LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE  300
Sbjct   241    LGNIVPGTEQVSQ+T+DGKDVYTTISS LQSFMETQMDAF EKVKGKYMTATLVSAKTGE  300
        LGNIVPGTEQVSQQTVDGKDVYTTISS TLQSFMETQMDAFLEKVKGKYMTATLVSAKTGE

Query   301    ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN  360
Sbjct   301    ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN  360
        ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFN

Query   361    SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK  420
Sbjct   361    SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK  420
        SSEFKIADATTRDWDVNDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRFK

Query   421    FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI  480
Sbjct   421    FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI  480
        FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI

Query   481    SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP  540
Sbjct   481    SAIYD N+Q+ RKSQKEIVGNPNVSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP  540
        SAIYDTNNQSVRKSQKEIVGNPNVSKAAS+TRTNMILVGTDPYGTMYNHYTGPPIITVP

Query   541    GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL  600
Sbjct   541    GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL  600
        GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPANPDFILYVTVQQPEHYSGIQL

Query   601    GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP  660
Sbjct   601    GEFA PILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP  660
        GEFATPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP

Query   661    IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVPMYGTWKETAETLAKWLNIELEF  720
Sbjct   661    IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDK EEVPMYGTWKETAETLAKWLNIELEF  720
        IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKVEEVPDMPYGTWKETAETLAKWLNIELEF

Query   721    QGSGSTVQKQDVRANTAIKDIKKITLTLGD  750
Sbjct   721    QGSGSTVQKQDVRANTAIKDIKKITLTLGD  750

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>dbj|BAD00919.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750



Score = 1357 bits (3511), Expect = 0.0, Method: Composition-based stats.  
Identities = 699/750 (93%), Positives = 726/750 (96%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTK+VIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQV Q+T+DGKDVYTTISS LQSFMETQM+AFQEKVKGKMYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEG+T+DFVWRDILYQSNYEPGSTMKVM LAAIDNNTFPGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIAD TIRDWDVNEGLTGGRMMTFSQGF SSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SA+YDPNDQ+ RKSQKEIVGNPVSKEAAS+TR MV+VGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLT+YIFSAVSM+PAENPDFILYVTVQQPEHYSIGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERA AMKDSLNLQ+TAKAL+Q+S Q+ Y MPS+KDISPGDLAEELRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVPMYGTWKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PDMYGW KETAET AKWL+IELEF	720
Query	721	QGS GSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	

>gb|AA17264.1|AF210754\_1 penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1349 bits (3492), Expect = 0.0, Method: Composition-based stats.  
Identities = 696/750 (92%), Positives = 725/750 (96%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTK+VIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KNGNGITYANMM+IKKELEAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQ+T+DGKDVYTTISS LQSFMETQM+AFQEKVKGKMYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEG+T+DFVWRDILYQSNYEPGSTMKVM LAAIDNNTFPGGEVFN	360

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-Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSELK+ADATIRDWDVNEGLTGG MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
SSELKVADATIRDWDVNEGLTGGGMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420

-Query 421 FGVPTREFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FG+PTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
FGIPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 +A+YDPN+Q+ RKSQKEIVGNPNVSKDAAS TRT+MVLVGTDP YGTMYNHSTGK TV VP 540
TALYDPNNQSVRKSQKEIVGNPNVSKDAASQTRTHMVLVGTDPVYGTMYNHSTGKATVNV 540

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVALKSGTA+IADEKNGGYLVG T++IFS V+M+PAENPDFILYVTVQQPEHYSGIQL 600
GQNVALKSGTAEIADEKNGGYLVGSTNHI FSVVAMNPAENPDFILYVTVQQPEHYSGIQL 600

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFANPILERA AMKDSLNLQ+TAK L+QV+ QS Y MPS+KDISPGDLAE LRRN+VQP 660
GEFANPILERAVAMKDSLNLQSTAKTLDQVTNQSAYAMPSIKDISPGDLAEALRRNIVQP 660

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLLISDKAEVDPMYGWTKEAETLAKWLNIELEF 720
Sbjct 661 IVVGTGTKIK SS EEG NLAPNQVLL+LSDKAEVDPMYGWTK TAE +KWLNIEL F 720
IVVGTGTKIKESSVEEGSNLAPNQVLLLSDKAEVDPMYGWTKATAEAFSKWLNIELVF 720

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 +GSGSTVQKQDVRANTAIKDIKKITLTLGD 750
EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

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>dbj|BAD00929.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1348 bits (3489), Expect = 0.0, Method: Composition-based stats.  
Identities = 695/750 (92%), Positives = 724/750 (96%), Gaps = 0/750 (0%)

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Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTK+VIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK 60
MKWTKKVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAVFLVNFAVIIGTGTRFGTDLAK 60

Query 61 EAKKVHQTTRTVPKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQTTRTVPKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
EAKKVHQTTRTVPKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KNGITYANMMSIKKELE AEVKGIDF 180
KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGSKNGITYANMMSIKKELETAEVKGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR 240
TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGKDGIIITYEKDR 240

Query 241 LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQ+T+DGKDVYTTISS LQSFMETQ+AFQEKVKGYMTATLVSAKTGE 300
LGNIVPGTEQVSQQTVVDGKDVYTTISS TLQSFMETQMNAFQEKVKGYMTATLVSAKTGE 300

Query 301 ILATTQRPFTFADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPFTFADTKEGIT+DFVWRDILYQSNYEPGSTMKVM LAAIDNNTFPGGEVFN 360
ILATTQRPFTFADTKEGITKDFVWRDILYQSNYEPGSTMKVMTLAAIDNNTFPGGEVFN 360

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSELKIAD TIRDWDVN+GLT GRMMTF QGFA SSNVGM+LLEQKMGDATWLDYLNRFK 420
SSELKIADVTIRDWDVNDGLTTGRMMTFLQGFA LSSNVGMSLLEQKMGDATWLDYLNRFK 420

Query 421 FGVPTREFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTREFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480
FGVPTREFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNH TGKP +TVP 540
SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNHQTGKPIITVP 540

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYS +QL 600
GQNVAVKSGTAQIADEKNGGYLVGSTNYIFS VVTMNPENPDFILYVTVQQPEHYS AVQL 600

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEF+NPILERASAMK+SLNLQ+ AK L+QV+ +S Y MPS+KDISPGDLAE LRRN+VQP 660
GEFSNPILERASAMKESLNLQSPAKNLDQVTTESSYAMPSIKDISPGDLAEALRRNIVQP 660

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLLISDKAEVDPMYGWTKEAETLAKWLNIELEF 720
Sbjct 661 IVVGTGTKIK +S EEGKNLAPNQVLL+LSDK EE+PDYMGWTK TAE +KWLNIEL F 720
IVVGTGTKIKETSVEEGKNLAPNQVLLLSDKVEEIPDYGWTKATAEAFSKWLNIELVF 720

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 +GSGSTVQKQDVRANTAIKDIKKITLTLGD 750

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Sbjct 721 EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

>dbj|BAD00909.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1345 bits (3481), Expect = 0.0, Method: Composition-based stats.  
Identities = 693/750 (92%), Positives = 720/750 (96%), Gaps = 0/750 (0%)


Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLLSDKAEVDPMYGWTKEATLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLLSDKAEVDPMYGWTKEATLAKWLNIELEF	720
Query	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	


>dbj|BAD00907.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1344 bits (3478), Expect = 0.0, Method: Composition-based stats.  
Identities = 691/750 (92%), Positives = 721/750 (96%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300

Sbjct	241	LGNI VPGTEQVSQRTMDGKD VYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFP GGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEG+T+DFVWRDILYQSNYEPGSTMKVM LA++IDNNTFP GE FN	360
Sbjct	301	ILATTQRPTFDADTKEGLT KDFVWRDILYQSNYEPGSTMKVM TLASSIDNNTFP SGEYFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIAD TIRDWDVN+GLT GRMMTF QGFA SSNVGM+LLEQKMGD TWLDYLNRFK	420
Sbjct	361	SSELKIADV TIRDWDVNDGLTTGRMMTFLQG FALSSNVGMSLLEQKMGDTTWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTV	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVG PVS+DAASLRTNM+LVGTDP+YGTMYNH TGKP +TV	540
Sbjct	481	SAIYDTNNQSVRSQKEIVGKPVSEDAASLRTNMILVGTDP IYGTMYNHYTGKPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNV A+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNP AENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMK+SLNLQ+ AK L+QV+ +S Y MPS+KDISPGDLAE LRRN+VQP	660
Sbjct	601	GEFANPILERASAMKESLNLQSPAKNLDQVTTESYAMPSIKDISPGDLAEALRRNIVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEV PDMYGWTKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK +S EEGKNLAPNQV L+LSDK EE+PDMYGW KETAET AKWL+IELEF	720
Sbjct	661	IVVGTGTKIKETSVEEGKNLAPNQVLLLSDKVEEI PDMYGWKKETAETFAKWL DIELEF	720
Query	721	QGS GSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	
Sbjct	721	EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750	

>pdb|1QME|A  Chain A, Penicillin-Binding Protein 2x (Pbp-2x)

    pdb|1QMF|A  Chain A, Penicillin-Binding Protein 2x (Pbp-2x) Acyl-Enzyme Complex  
Length=702

Score = 1344 bits (3478), Expect = 0.0, Method: Composition-based stats.  
Identities = 702/702 (100%), Positives = 702/702 (100%), Gaps = 0/702 (0%)

Query	49	GTGTRFGTDLAKEAKKVHQTTRTPVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT	108
Sbjct	1	GTGTRFGTDLAKEAKKVHQTTRTPVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT	60
Sbjct	1	GTGTRFGTDLAKEAKKVHQTTRTPVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT	60
Query	109	GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGGITYANMMSIKK	168
Sbjct	61	GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGGITYANMMSIKK	120
Sbjct	61	GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGGITYANMMSIKK	120
Query	169	ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA	228
Sbjct	121	ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA	180
Sbjct	121	ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA	180
Query	229	GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD VYTTISSPLQSFMETQMDAFQEKVKGKY	288
Sbjct	181	GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD VYTTISSPLQSFMETQMDAFQEKVKGKY	240
Sbjct	181	GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD VYTTISSPLQSFMETQMDAFQEKVKGKY	240
Query	289	MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI	348
Sbjct	241	MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI	300
Sbjct	241	MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI	300
Query	349	DNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG	408
Sbjct	301	DNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG	360
Sbjct	301	DNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG	360
Query	409	DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAI	468
Sbjct	361	DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAI	420
Sbjct	361	DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAI	420
Query	469	ANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMY	528
Sbjct	421	ANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMY	480
Sbjct	421	ANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMY	480
Query	529	NHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT	588
Sbjct	481	NHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT	540
Sbjct	481	NHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT	540
Query	589	VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGD	648
Sbjct	541	VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGD	600
Sbjct	541	VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGD	600
Query	649	LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEV PDMYGWTKETAET	708
Sbjct	649	LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEV PDMYGWTKETAET	708
Sbjct	649	LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEV PDMYGWTKETAET	708

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Sbjct 601 LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEVDPMYGWTKETAE 660
Query 709 TLAKWLNIELEFQGGSGSTVQKQDV RANTAIKDIKKITLTLGD 750
        TLAKWLNIELEFQGGSGSTVQKQDV RANTAIKDIKKITLTLGD
Sbjct 661 TLAKWLNIELEFQGGSGSTVQKQDV RANTAIKDIKKITLTLGD 702
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>pdb|1PYY|A Chain A, Double Mutant Pbp2x T338aM339F FROM STREPTOCOCCUS Pneumoniae  
Strain R6 At 2.4 A Resolution  
Length=702

Score = 1341 bits (3471), Expect = 0.0, Method: Composition-based stats.  
Identities = 700/702 (99%), Positives = 700/702 (99%), Gaps = 0/702 (0%)

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Query 49 GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 108
Sbjct 1 GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 60

Query 109 GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKK 168
Sbjct 61 GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKK 120

Query 169 ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 228
Sbjct 121 ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 180

Query 229 GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKY 288
Sbjct 181 GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKY 240

Query 289 MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI 348
Sbjct 241 MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGS KVMMLAAAI 300

Query 349 DNNTFPGGEVFNSSELKIADATIRDWVDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMG 408
Sbjct 301 DNNTFPGGEVFNSSELKIADATIRDWVDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMG 360

Query 409 DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAI 468
Sbjct 361 DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAI 420

Query 469 ANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAASLTRTNMVLVGTDPVYGTM 528
Sbjct 421 ANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAASLTRTNMVLVGTDPVYGTM 480

Query 529 NHSTGKPTVTVPQGQNALVSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT 588
Sbjct 481 NHSTGKPTVTVPQGQNALVSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT 540

Query 589 VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGD 648
Sbjct 541 VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGD 600

Query 649 LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEVDPMYGWTKETAE 708
Sbjct 601 LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEVDPMYGWTKETAE 660

Query 709 TLAKWLNIELEFQGGSGSTVQKQDV RANTAIKDIKKITLTLGD 750
Sbjct 661 TLAKWLNIELEFQGGSGSTVQKQDV RANTAIKDIKKITLTLGD 702
```

>dbj|BAD00918.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1340 bits (3469), Expect = 0.0, Method: Composition-based stats.  
Identities = 692/750 (92%), Positives = 718/750 (95%), Gaps = 0/750 (0%)

```
Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAV IIGTGTRFGTDLAK 60
Sbjct 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAV IIGTGTRFGTDLAK 60

Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
```

Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFP GGGEVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYMPSPVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERA AMKDSLNLQ+TAK L+QV+ QS Y MPS+KDISPGDLAE LRRN+VQP	660
Query	661	IVVGTGTGKIKNSSAEEGKNLAPNQVLLISDKAEVVPD MYGWTKETAE TLAKWLNIELEF	720
Sbjct	661	IVVGTGTGKIK SS EEG NLAPNQVLL+LSDKAEVVPD MYGWT KAEAFSKWLNIELVF	720
Query	721	QGS GSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	+GSGSTVQKQDVRANTAIKDIKKITLTLGD 750	

>dbj|BAD00910.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1336 bits (3458), Expect = 0.0, Method: Composition-based stats.  
Identities = 690/750 (92%), Positives = 719/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFP GGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVA+KSGTAQIADEKNGGYLVG T+YIFS AV+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYMPSPVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660

```

-Query 661  IVVGTGTKIKNSSAEEGKNLAPNQVLLSDDKAEVDPMYGWTKEAETLAKWLNIELEF 720
              IVVGTGTKIK SS EEG NLAPNQVLL+LSDKAEVDPMYGWTKEAETLAKWLNIELEF 720
Sbjct 661  IVVGTGTKIKESSVEEGTNLAPNQVLLSDDKAEVDPMYGWTKEAETLAKWLNIELEF 720

-Query 721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
              +GSGSTVQKQDVRANTAIKDIKKITLTLGD
Sbjct 721  EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

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>dbj|BAD00923.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
dbj|BAD00924.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
dbj|BAD00934.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

```

Score = 1327 bits (3433), Expect = 0.0, Method: Composition-based stats.  
Identities = 683/750 (91%), Positives = 716/750 (95%), Gaps = 0/750 (0%)

```

Query 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180

Query 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSMESSLSNLAGTDGIITYEKDR 240
Sbjct 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSMESSLSNLAGTDGIITYEKDR 240

Query 241    LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241    LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFLEKVKGYMTATLVSAKTGE 300

Query 301    ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN 360
Sbjct 301    ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN 360

Query 361    SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361    SSEFKIADATTRDWDVNDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLNRFK 420

Query 421    FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421    FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480

Query 481    SAIYDPNDQTARKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481    SAIYD N+Q+ RKSQKEIVGNPVSKEAAS TR +M+LVGTDP+YGTMYNH TGKP +TVP 540

Query 541    GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQOPEHYSGIQL 600
Sbjct 541    GQNV+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQOPEHYSGIQL 600

Query 601    GEFANPILERASAMKDSLNLOTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601    GEFA PILERASAMK+SLNLO+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP 660

Query 661    IVVGTGTKIKNSSAEEGKNLAPNQVLLSDDKAEVDPMYGWTKEAETLAKWLNIELEF 720
Sbjct 661    IVVGTGTKIK+SS EEG NLAPNQVLL+LSDK EE+PDYMGW KETAET AKWL+IELEF 720

Query 721    QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
              +GSGS VQKQDVR NTAIK+IKKITLTLGD
Sbjct 721    EGSGSVVQKQDVRTNTAIKNIKKITLTLGD 750

```

```

>dbj|BAD00917.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

```

Score = 1324 bits (3427), Expect = 0.0, Method: Composition-based stats.  
Identities = 680/750 (90%), Positives = 717/750 (95%), Gaps = 0/750 (0%)

```

Query 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180

```



```

- Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KGNNGITYANMM+IKKELE AEVKGIDF 180
Query 181 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGSKGNNGITYANMMAIKKELETAEVKGIDF 240
- Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Query 241 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 241 LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE 300
Query 241 LGNIVPGTEQVSQ+T+DGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQQTVDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE 300
Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTFDADTKEG+T+DFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN 360
Query 361 ILATTQRPTFDADTKEGTLTKDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFN 360
Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVN+GLT G MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RFK 420
Query 421 SSEFKIADATTRDWDVNDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFK 420
Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480
Query 481 FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480
Query 481 SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP 540
Query 541 SAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRNHMILVGTDPVYGTMYNHSTGKPIITVP 540
Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL 600
Query 601 GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPANPDFILYVTVQQPEHYSGIQL 600
Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPGDLAE LRRN+VQP 660
Query 661 GEFATPILERASAMKESLNLQSPAKNLDKVTTESYAMPSIKDISPGDLAEALRRNIVQP 660
Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLLISDKAEVDPMYGWTAKETLAKWLNIELEF 720
Sbjct 661 IVVGTGTKIK +S EEGKNLAPNQVLL+LSDK EE+PDYMGW KETAET AKWL+IELEF 720
Query 721 IVVGTGTKIKETSVEEGKNLAPNQVLLLSDKVEEIPDYGWKKETAETFAKWLDIELEF 720
Query 721 QGSGSTVQKQDVRANTAIKDIKITLTLGD 750
Sbjct 721 +GSGS VQKQDVR NTAIK+IKKI LTLGD 750
Query 721 EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750

```

>dbj|BAD00927.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1323 bits (3425), Expect = 0.0, Method: Composition-based stats.  
Identities = 681/750 (90%), Positives = 715/750 (95%), Gaps = 0/750 (0%)

```

Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF 180
Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR 240
Query 241 LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQ+T+DGKDVTYTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGE 300
Query 301 LGNIVPGTEQVSQQTVDGKDVTYTTLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGE 300
Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN 360
Query 361 ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFN 360
Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVNEGLT G MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RFK 420
Query 421 SSEFKIADATTRDWDVNEGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFK 420
Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480
Query 481 FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480
Query 481 SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP 540
Query 481 SAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRNHMILVGTDPVYGTMYNHSTGKPIITVP 540

```



```

Query   541  GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL  600
      -  GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL
Sbjct   541  GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPENPDFILYVTVQQPEHYSGIQL  600

Query   601  GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP  660
      -  GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPGDLAEELRRN+VQP
Sbjct   601  GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGDLAEELRRNIVQP  660

Query   661  IVVGTGTHIKNSSAEEGKNLAPNQVLLILSDKAEVDPMYGWTKEAETLAKWLNIELEF  720
      -  IVVG GTHIK +S EEG NLAPNQVLL+LSDK EE+PDYMGW KETAET AKWL+IELEF
Sbjct   661  IVVGAGTHIKETSVEEGTNLAPNQVLLILSDKVEEIPDYGWKKETAETFAKWLIDIELEF  720

Query   721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD  750
      +GSGS VQKQDVR NTAIK+IKKI LTLGD
Sbjct   721  EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD  750

```

>dbj|BAD00913.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1318 bits (3410), Expect = 0.0, Method: Composition-based stats.  
Identities = 677/750 (90%), Positives = 714/750 (95%), Gaps = 0/750 (0%)

```

Query   1    MKWTKRVIRYATKNRKSAPENRRRVGKSLSLLSVVFVFAIFLVNFAVIIGTGTRFGTDLAK  60
      -  MKWTKRVIRYATKNRKSAPENRRRVGKSLSLLSVVFVFA+FLVNFAVIIGTGTRFGTDLAK
Sbjct   1    MKWTKRVIRYATKNRKSAPENRRRVGKSLSLLSVVFVFAVFLVNFAVIIGTGTRFGTDLAK  60

Query   61    EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN  120
      -  EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN
Sbjct   61    EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN  120

Query   121   KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF  180
      -  KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMM+IKKELE AEVKGIDF
Sbjct   121   KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMAIKKELETAEVKGIDF  180

Query   181   TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSMESSLNSILAGTDGIITYEKDR  240
      -  TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSMESSLNSILAG DGIITYEKDR
Sbjct   181   TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSMESSLNSILAGKDGIIITYEKDR  240

Query   241   LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE  300
      -  LGNIVPGTEQVSQ+T+DGKDVYTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGE
Sbjct   241   LGNIVPGTEQVSQQTVDGKDVYTTLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGE  300

Query   301   ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN  360
      -  ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN
Sbjct   301   ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFN  360

Query   361   SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK  420
      -  SSE KIADAT RDWDVNEGLT G MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RFK
Sbjct   361   SSEFKIADATTRDWDVNEGLTTGGMMTFLQGFHSSNVGMSLLEQKMGDATWLDYLRFK  420

Query   421   FGVPTREFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI  480
      -  FGVPTREFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI
Sbjct   421   FGVPTREFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI  480

Query   481   SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP  540
      -  SAIYD N+Q+ RKSQKEIVGNPVSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP
Sbjct   481   SAIYDTNNQSVRKSQKEIVGNPVSKAAASTTRNHMILVGTDPPLYGTMYNHYTGPPIITVP  540

Query   541  GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL  600
      -  GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL
Sbjct   541  GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPENPDFILYVTVQQPEHYSGIQL  600

Query   601  GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP  660
      -  GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP
Sbjct   601  GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQP  660

Query   661  IVVGTGTHIKNSSAEEGKNLAPNQVLLILSDKAEVDPMYGWTKEAETLAKWLNIELEF  720
      -  IVVGTHIKIK +S EEG NLAPNQVLL+LSDK EE+PDYMGW KETAET AKWL+IELEF
Sbjct   661  IVVGTHIKIKETSVEEGTNLAPNQVLLILSDKVEEIPDYGWKKETAETFAKWLIDIELEF  720

Query   721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD  750
      +GSGS VQKQDVR NTAIK+IKKI LTLGD
Sbjct   721  EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD  750

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>dbj|BAD00938.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1316 bits (3407), Expect = 0.0, Method: Composition-based stats.  
Identities = 676/750 (90%), Positives = 713/750 (95%), Gaps = 0/750 (0%)

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Query   1    MKWTKRVIRYATKNRKSAPENRRRVGKSLSLLSVVFVFAIFLVNFAVIIGTGTRFGTDLAK  60
      -  MKWTKRVIRYATKNRKSAPENRRRVGKSLSLLSVVFVFA+FLVNFAVIIGTGTRFGTDLAK
Sbjct   1    MKWTKRVIRYATKNRKSAPENRRRVGKSLSLLSVVFVFAVFLVNFAVIIGTGTRFGTDLAK  60

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Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLQVSFGAKNGITYANMMAIKKELETAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGDKDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKDVYTTLSSPLQSFMETQMDAFLEKVKGKMYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVMMLA++IDNNTFP GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSEKIADATRDWDVNEGLTGMMTFQGFAHSSNVGM+LLEQKMGDATWLDYLRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPNVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTV	540
Sbjct	481	SAIYDNNQ+RKSQKEIVGNPNVSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TV	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPENPDFILYVTVQQPEHYSIGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYMPSPVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLLSDKAEVPMYGWTKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPMYGWKKETAETFAKWLDIELEF	720
Query	721	QGSGSTVQKQDVRANTAIDIKKITLTLGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	

>dbj|BAD00922.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1316 bits (3405), Expect = 0.0, Method: Composition-based stats.  
Identities = 678/750 (90%), Positives = 713/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELETAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGDKDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKDVYTTISSPLQSFMETQMDAFLEKVKGKMYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSEKIADATRDWDVNEGLTGMMTFQGFAHSSNVGM+LLEQKMGDATWLDYLRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480

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- Query  481  SAIYDPNDQTARKSQKEIVGNPVSKDAA SLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP  540
          SAIYD N+Q+ RKSQKEIVGNPVS KAAS TR +M+LVGTDP+YGTMYNH TGKP +TVP
Sbjct  481  SAIYDTNNQSVRKSQKEIVGNPVSKEAAS TRNHMILVGTDP LYGTMYNHYTGKPIITVP  540

- Query  541  GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL  600
          GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL
Sbjct  541  GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNP AENPDFILYVTVQQPEHYSGIQL  600

Query  601  GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP  660
          GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP
Sbjct  601  GEFATPILERASAMKESLNLQSPAKNLDKVTTESYAMPSIKDISPGELAEALRRNIVQP  660

Query  661  IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPMYGWT KETAETLAKWLNIELEF  720
          IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PD MYGW KETAET AKWL+IELEF
Sbjct  661  IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPD MYGWKKETAETFAKWLDIELEF  720

Query  721  QGSGSTVQKQDV RANTAIKDIKKITLTLGD  750
          +GSGS VQKQDVR NTAIK+IKKI LTLGD
Sbjct  721  EGSGSVVQKQDV RTNTAIKNIKKIKLTLGD  750

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>dbj|BAD00925.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1315 bits (3403), Expect = 0.0, Method: Composition-based stats.  
Identities = 676/750 (90%), Positives = 712/750 (94%), Gaps = 0/750 (0%)

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Query  1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK  60
          MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK
Sbjct  1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAVFLVNFAVIIGTGTRFGTDLAK  60

Query  61      EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN  120
          EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN
Sbjct  61      EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN  120

Query  121     KVAEVFHKYLDMEESYVREQLSQPNLQVVSFGAKGNGITYANMMSIKKELEAAEVKGIDF  180
          KVAEVFHKYLDMEESYVREQLSQPNLQVVSFGAKGNGITYANMMSIKKELE AEVKGIDF
Sbjct  121     KVAEVFHKYLDMEESYVREQLSQPNLQVVSFGAKGNGITYANMMSIKKELETAEVKGIDF  180

Query  181     TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR  240
          TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR
Sbjct  181     TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGKDGIITYEKDR  240

Query  241     LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVS AKTGE  300
          LGNIVPGTEQVSQ+T+DGKDVYTT+SSPLQSFMETQMDAF EKVKGKYMTATLVS AKTGE
Sbjct  241     LGNIVPGTEQVSQQTVDGKDVYTTLSPLQSFMETQMDAFLEKVKGKYMTATLVS AKTGE  300

Query  301     ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFP GGEVFN  360
          ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVMMLA++IDNNTFP GE FN
Sbjct  301     ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGS AFKVMMLASSIDNNTFP SGEYFN  360

Query  361     SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK  420
          SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK
Sbjct  361     SSEFKIADATTRDWDVNEGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRFK  420

Query  421     FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAF TA IANDGVMLEPKFI  480
          FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTA IANDGVMLEPKFI
Sbjct  421     FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTA IANDGVMLEPKFI  480

Query  481     SAIYDPNDQTARKSQKEIVGNPVSKDAA SLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP  540
          SAIYD N+Q+ RKSQKEIVGNPVS KAAS TR +M+LVGTDP+YGTMYNH TGKP +TVP
Sbjct  481     SAIYDTNNQSVRKSQKEIVGNPVSKEAAS TRNHMILVGTDP LYGTMYNHYTGKPIITVP  540

Query  541     GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL  600
          GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQ
Sbjct  541     GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNP AENPDFILYVTVQQPEHYSGIQS  600

Query  601     GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP  660
          GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP
Sbjct  601     GEFATPILERASAMKESLNLQSPAKNLDKVTTESYAMPSIKDISPGELAEALRRNIVQP  660

Query  661     IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPMYGWT KETAETLAKWLNIELEF  720
          IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PD MYGW KETAET AKWL+IELEF
Sbjct  661     IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPD MYGWKKETAETFAKWLDIELEF  720

Query  721     QGSGSTVQKQDV RANTAIKDIKKITLTLGD  750
          +GSGS VQKQDVR NTAIK+IKKI LTLGD
Sbjct  721     EGSGSVVQKQDV RTNTAIKNIKKIKLTLGD  750

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>dbj|BAD00926.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1315 bits (3402), Expect = 0.0, Method: Composition-based stats.  
Identities = 676/750 (90%), Positives = 714/750 (95%), Gaps = 0/750 (0%)

- Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTK+VIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK	60
- Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300
Sbjct	241	+GNIVPGTE VSQ+T+DGKDVTYTT+SSPLQSFMETQMDAF EKVKGKMYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTF GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVSKEAAS TR +M+LVGTDP+YGTMYNH TGKP +TVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLISDKAEVVPDYGWTKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK+S EEG NLAPNQVLL+LSDK EE+PDYGW KETAET AKWL+IELEF	720
Query	721	QGSGSTVQKQDVRRNTAIKDIKITLTLGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	

>gb|AA17268.1|AF210758\_1 penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1313 bits (3398), Expect = 0.0, Method: Composition-based stats.  
Identities = 675/750 (90%), Positives = 713/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KNGITYANMMSIKKELEAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300
Sbjct	241	+GNIVPGTE VSQ+T+DGKDVTYTT+SSPLQSFMETQMDAF EKVKGKMYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTF GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420

Sbjct	361	SSEFKIADATTRDWDVNDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRKF	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSFDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVS+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGEALAEALRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLISDKAEVDPMYGWTKEAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIKETSVEEGTNLAPNQVLLISDKVEEIPDMYGWKKETAETFAKWLIDIELEF	720
Query	721	QSGGSTVQKQDVRRNTAIKDIKKITLTLGD	750
Sbjct	721	EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD	750

>gb|AAFI7270.1|AF210760\_1 penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1312 bits (3396), Expect = 0.0, Method: Composition-based stats.  
Identities = 673/750 (89%), Positives = 713/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSAPENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKKRVIRYATKNRKSAPENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRIVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMAIKKELETAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKDVYTTLSPLQSFMETQMDAFLEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTF GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLRNFK	420
Sbjct	361	SSEKIADATRDWDVN+GLT G MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSFDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVS+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGEVAEALRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLISDKAEVDPMYGWTKEAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIKETSVEEGTNLAPNQVLLISDKVEEIPDMYGWKKETAET AKWL+IELEF	720
Query	721	QSGGSTVQKQDVRRNTAIKDIKKITLTLGD	750
Sbjct	721	EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD	750

>dbj|BAD00932.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1312 bits (3396), Expect = 0.0, Method: Composition-based stats.  
Identities = 673/750 (89%), Positives = 712/750 (94%), Gaps = 0/750 (0%)

Query	1	MKWTKR VIRYATK NRKSPAENRRRVGKSL SLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKR VIRYATK NRKSPAENRRRVGKSL SLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELE AEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQ+T+DGKDVYTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFPGGGEVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVMMLA++IDNNTFP GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTD P+YGTMYNH TGKP +TVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHITSVQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEF+NPILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVVPD MYGWT KETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PD MYGW KETAET AKWL+IELEF	720
Query	721	QSGSGSTVQKQDVRANTAIKDIKITLTLGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	

>gb|AAF17269.1|AF210759\_1 penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1312 bits (3395), Expect = 0.0, Method: Composition-based stats.  
Identities = 674/750 (89%), Positives = 712/750 (94%), Gaps = 0/750 (0%)

Query	1	MKWTKR VIRYATK NRKSPAENRRRVGKSL SLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKR VIRYATK NRKSPAENRRRVGKSL SLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGN GITYANMMSIKKELE AEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQ+T+DGKDVYTT+SSPLQSFMETQMDAF +KVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFPGGGEVFN	360

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- Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNEYEPGS KVM LA++IDNNTFP GE FN 360
ILATTQRPTFNADTKEGITEDFVWRDILYQSNEYEPGSFAKVMTLASSIDNNTFPSGEYFN
Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
SSE KIADAT RDWDVN GLT G MMTF SQGFAHSSNVG +LLEQKMGDATWLDYL RFK
- Sbjct 361 SSEFKIADATTRDWDVNAGLTTGGMMTFSQGFAHSSNVGTSLLEQKMGDATWLDYLKRFK 420
Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFI 480
FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480
Query 481 SAIYDPNDQTARKSQKEIVGNPVSFDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTV 540
SAIYD N+Q+ RKSQKEIVGNPVS+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP
Sbjct 481 SAIYDTNNQSGRKSQKEIVGNPVSKEAASSTRNHMILVGTDPVYGTMYNHSTGKPIITVP 540
Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL 600
GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEH+SGIQL
Sbjct 541 GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPANPDFILYVTVQQPEHFSGIQL 600
Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP
Sbjct 601 GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQP 660
Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPMYGWTKETATLAKWLNIELEF 720
IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PDYMGW KETAT AKWL+IELEF
Sbjct 661 IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPDYGWKKETATFAKWLDIELEF 720
Query 721 QGSGSTVQKQDVRRANTAIKDIKKITLTLGD 750
+GSGS VQKQDVR NTAIK+IKKI LTLGD
Sbjct 721 EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750

```

>dbj|BAD00936.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1312 bits (3395), Expect = 0.0, Method: Composition-based stats.  
Identities = 675/750 (90%), Positives = 712/750 (94%), Gaps = 0/750 (0%)

```

Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK 60
Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQTTTR VPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELETAEVKGIDF 180
Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAG DGIITYEKDR 240
Query 241 LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQQTVDGKDVTYTTISSTLQSFMETQMDAFLEKVKGYMTATLVSAKTGE 300
Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYEPGSTMKVMMLAAIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNEYEPGS MKVM LA++IDNNTFP GE FN 360
Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL+RFK
Sbjct 361 SSEFKIADATTRDWDVNDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLSRFK 420
Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFI 480
FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480
Query 481 SAIYDPNDQTARKSQKEIVGNPVSFDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTV 540
SAIYD N+Q+ RKSQKEIVGNPVS+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP
Sbjct 481 SAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRNHMILVGTDPVYGTMYNHSTGKPIITVP 540
Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL 600
GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSIGIQL
Sbjct 541 GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPANPDFILYVTVQQPEHYSIGIQL 600
Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP
Sbjct 601 GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQP 660
Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPMYGWTKETATLAKWLNIELEF 720
IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PDYMGW KETAT AKWL+IELEF
Sbjct 661 IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPDYGWKKETATFAKWLDIELEF 720

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Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
+GSGS VQKQDVR NTAIK+IKKI LTLGD
Sbjct 721 EGSGSVQKQDVRTNTAIKNIKKIKLTLGD 750

```

>gb|AAL77081.1|AF468152\_1 penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1307 bits (3382), Expect = 0.0, Method: Composition-based stats.  
Identities = 667/750 (88%), Positives = 711/750 (94%), Gaps = 0/750 (0%)

```

Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKR+ R+A +NRKSPAENR+ VGK +SLL+V +FA+FLVNFAVIIG+G++FGTDL K
MKWTKRITRFAIRNRKSPAENRKIVGKYISLLAVVLFAVFLVNFAVIIGSGSKFGTDLVK 60

Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQ TRTPAKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN
EAKKVHQITRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEAYVKEQLAQPNLTQVSFGAKGNGITYANMMAIKKDKDASVEGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR
TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGKDGIIITYEKDR 240

Query 241 LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQ+T+DGKDVYTTISS LQSFMETQM+AFQEKVKGYMTATLVSAKTGE
LGNIVPGTEQVSQQTVDGKDVYTTISSSTLQSFMETQMNAFQEKVKGYMTATLVSAKTGE 300

Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYEPGSTMKVMMLAAAI DNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTFDADTKEG+T+DFVWRDILYQSNEYEPGSTMKVM LAAAI DNNTFPGGEVFN
ILATTQRPTFDADTKEGLTKDFVWRDILYQSNEYEPGSTMKVMTLAAAI DNNTFPGGEVFN 360

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGF AHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSELKIAD TIRDWDVNEGLTGGRMMTFSQGF A SSNVGMTLLEQKMGDATWLDYLNRFK
SSELKIADVTIRDWDVNEGLTGGRMMTFSQGFALSSNVGMTLLEQKMGDATWLDYLNRFK 420

Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI
FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDVPYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVG PVS+DAASLRTNM+LVGTD+YGTMYNH TGKP +TVP
SAIYDTNNQSVRKSQKEIVGKPVSEDAASLRTNMILVGTDPLYGTMYNHQTGKPIITVP 540

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL
GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPANPDFILYVTVQQPEHYSGIQL 600

Query 601 GEFANPILERASAMKDSLNLOTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFANPILERA AMKDSLNLO+TAK L+QV+ QS Y MPS+KDISPGDLAE LRRN+VQP
GEFANPILERAVAMKDSLNLOSTAKTLDQVTNQ SAYAMPSIKDISPGDLAEALRRNIVQP 660

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF 720
Sbjct 661 IVVGTGTKIK SS EEG NLAPNQVLL+LSDKAEVDPMYGWT KAE +KWLNIEL F
IVVGTGTKIKESSVEEGTNLAPNQVLLLSLKAEVDPMYGWT KATAEAFSKWLNIELVF 720

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
+GSGSTVQKQDVRANTAIKDIKKI LTLGD
Sbjct 721 EGSGSTVQKQDVRANTAIKDIKKIKLTLGD 750

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>dbj|BAD00939.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1307 bits (3382), Expect = 0.0, Method: Composition-based stats.  
Identities = 670/750 (89%), Positives = 711/750 (94%), Gaps = 0/750 (0%)

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Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTK+VIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK
MKWTKKVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAVFLVNFAVIIGTGTRFGTDLAK 60

Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQ TRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN
EAKKVHQITRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KNGNGITYANMM+IKKELE AEVKGIDF
KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGSKGNGITYANMMAIKKELETAEVKGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR
TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240

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Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	+GNIVPGTE VSQ+T+DGKDVYTT+SSPLQSFMETQMDAF +KVKGYMTATLVSAKTGE VGNIVPGTELVSQQTVDGKDVYTTLSSPLQSFMETQMDAFLQKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVMMLA++IDNNTFP GE FN ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSFAKVMMLASSIDNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVNEGLT G MMTF QGFHSSNVG +LLEQKMGDATWLDYL RFK SSEFKIADATTRDWDVNEGLTTGGMMTFLQGFHSSNVGTSLLEQKMGDATWLDYLRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPNVSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP SAIYDTNNQSVRKSQKEIVGNPNVSKEAASSTRNHMILVGTDPPLYGTMYNHYTGKPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLILSDKAEVPMYGTWKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK +S EEG NLAPNQVL+LSDK EE+PDYMGW KETAET AKWL+IELEF IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPDYGWKKETAETFAKWLIDIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750	

>dbj|BAD00935.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1306 bits (3380), Expect = 0.0, Method: Composition-based stats.  
Identities = 667/750 (88%), Positives = 715/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAVFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KNGGITYANMMSIKK+LE A+V+GIDF KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGSKGNGITYANMMSIKKDLETAKVEGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNG+FASSFIGLAQLHENEDGSKSL+GTSG+ESSLNS+LAGTDGIITYEKDR TTSPNRSYPNGKFASSFIGLAQLHENEDGSKSLIGTSGVESSLNSLLAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQV+++T++GKDVYTT+SSPLQSFME+QMDAFQEK+KGKGYMTATLVSAKTGE LGNIVPGTEQVTRQTVNGKDVYTTLSSPLQSFMESQMDAFQEKLGKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVNEGLT G MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RFK SSEFKIADATTRDWDVNEGLTTGGMMTFLQGFHSSNVGMSLLEQKMGDATWLDYLRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPNVSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP SAIYDTNNQSVRKSQKEIVGNPNVSKEAASSTRNHMILVGTDPPLYGTMYNHYTGKPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQP	660

```

Query 661  IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVPMYGWTKETAETLAKWLNIELEF 720
Sbjct 661  IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PDMYGW KETAET AKWL+IELEF
          IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPDMYGWKKETAETFAKWL DIELEF 720

Query 721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721  +GSGS VQKQDVR NTAIK+IKKI LTLGD
          EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750

```

>dbj|BAD00906.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1305 bits (3378), Expect = 0.0, Method: Composition-based stats.  
Identities = 669/750 (89%), Positives = 710/750 (94%), Gaps = 0/750 (0%)

```

Query 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN
          EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFN 120

Query 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KGNGITYANMM+IKKELE AEVKGIDF
          KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGSKGNGITYANMMAIKKELETAEVKGIDF 180

Query 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNILAGTDGIITYEKDR 240
Sbjct 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLN ILAGTDGIITYEKDR
          TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNRIILAGTDGIITYEKDR 240

Query 241    LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSACTGE 300
Sbjct 241    LGNIVPGTEQVSQ+T+DGKDVYTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSACTGE
          LGNIVPGTEQVSQQTVDGKDVYTTLSSPLQSFMETQMDAFLEKVKGKYMTATLVSACTGE 300

Query 301    ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAIIDNNTFPGGEVFN 360
Sbjct 301    ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN
          ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFN 360

Query 361    SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361    SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK
          SSEFKIADATTRDWDVNDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRFK 420

Query 421    FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421    FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI
          FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480

Query 481    SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481    SAIYD N+Q+ RKSQKEIVGNPVSK+AAS TR +M+LVGTD+YGTMYNH TGKP +TVP
          SAIYDTNNQSVRKSQKEIVGNPVSKAASTTRNHMILVGTDPFLYGTMYNHYTGPPIITVP 540

Query 541    GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541    GQNV+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL
          GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPANPDFILYVTVQQPEHYSGIQL 600

Query 601    GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601    GEFA PILERASAM+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP
          GEFATPILERASAMKESLNLQSPAKNLDKVTTESYAMPSIKDISPGELAEALRRNIVQP 660

Query 661    IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVPMYGWTKETAETLAKWLNIELEF 720
Sbjct 661    IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PDMYGW KETAET AKWL+IELEF
          IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPDMYGWKKETAETFAKWL DIELEF 720

Query 721    QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721    +GSGS VQKQDVR NTAIK+IKKI LTLGD
          EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750

```

>dbj|BAD00937.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1303 bits (3373), Expect = 0.0, Method: Composition-based stats.  
Identities = 664/750 (88%), Positives = 711/750 (94%), Gaps = 0/750 (0%)

```

Query 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61     EAKKVHQ TTTPAKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN
          EAKKVHQITRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFN 120

Query 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121    KVAEVFHKYLD+M+E+YV+EQL+QPNL QVSFGAKGNGITYANMM+IKK+L+ A V+GIDF
          KVAEVFHKYLDMEAYVKEQLAQPNLTQVSFGAKGNGITYANMMAIKKDLKDASVEGIDF 180

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Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSG+ESSLN+ILAGTDGIITYEKDR 240

Query 241 LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 +GNIVPGTE VSQ+T+DGKDVTYTT+SSPLQSFMETQMDAF EKVKGKGYMTATLVSAKTGE 300
Sbjct 241 VGNIVPGTELVSQQTVDGKDVTYTTLSSPLQSFMETQMDAFLEKVKGKGYMTATLVSAKTGE 300

Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFP GGGEVFN 360
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN 360
Sbjct 301 ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFN 360

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK 420
Sbjct 361 SSEFKIADATTRDWDVNEGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRFK 420

Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP 540
Sbjct 481 SAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRNHMILVGTDPVYGTMYNHSTGKPIITVP 540

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPANPDFILYVTVQQPEHYSGIQL 600

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEF PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPGDLAEELRRN+VQP 660
Sbjct 601 GEFVTPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGDLAEELRRNIVQP 660

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLLISDKAEVVPDMYGWTKETAETLAKWLNIELEF 720
Sbjct 661 IV+G GTKIKN+S EEGKNLAPNQVLL+LSDK EE+PDMYGWTK TAE +KWLNIELEF 720
Sbjct 661 IVIGAGTKIKNASIEEGKNLAPNQVLLLSDKVEEIPDMYGWTKTAEAFSKWLNIELEF 720

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 +GSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

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>pdb|1RP5|A Chain A, Pbp2x From Streptococcus Pneumoniae Strain 5259 With Reduced Susceptibility To Beta-Lactam Antibiotics

pdb|1RP5|B Chain B, Pbp2x From Streptococcus Pneumoniae Strain 5259 With Reduced Susceptibility To Beta-Lactam Antibiotics

emb|CAE53270.1| penicillin-binding protein 2x [Streptococcus pneumoniae] Length=702

Score = 1297 bits (3357), Expect = 0.0, Method: Composition-based stats.  
Identities = 674/702 (96%), Positives = 688/702 (98%), Gaps = 0/702 (0%)

```

Query 49 GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 108
Sbjct 1 GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 60

Query 109 GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKK 168
Sbjct 61 GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKK 120

Query 169 ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 228
Sbjct 121 ELEAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 180

Query 229 GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGY 288
Sbjct 181 GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGY 240

Query 289 MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI 348
Sbjct 241 MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI 300

Query 349 DNNTFP GGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKM 408
Sbjct 301 DNNTFP GGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKM 360

Query 409 DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAI 468
Sbjct 361 DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIA S+FGQGISVTQTQM+RAFTAI 420
Sbjct 361 DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIA S+FGQGISVTQTQMLRAFTAI 420

Query 469 ANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMY 528
Sbjct 421 ANDGVMLEPKFISALYDPNDQSVRKSQKEIVGNPVSKEAASVTRDHMMVMVGTDPYGTMY 480

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Query 529 NHSTGKPTVTVPQGQNALVKSQTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT 588
Sbjct 481 NHSTGK TV VPGQNALVKSQTA+IADEKNGGYL G T+ IFS VSM PAENPDFILYVT 540
NHSTGKATVNVPGQNALVKSQTAETIADEKNGGYLTGSTNNIFSVSMHPAENPDFILYVT

Query 589 VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGD 648
Sbjct 541 VQQPEHYSGIQLGEFANPILERASAMK+SLNLQTTAKALEQVSQQSPYPMPSVKDISPGD 600
VQQPEHYSGIQLGEFANPILERASAMKESLNLQTTAKALEQVSQQSPYPMPSVKDISPGD

Query 649 LAEELRRNLVQPIVVGTGTGIKNSAEEGKNLAPNQQVLILSDKAEVPMYGTWKETAETAE 708
Sbjct 601 LAEELRRNLVQPIVVGTGTGIKNSAEEGKNLAPNQQVLILSDKAEVPMYGTWKETAETAE 660
LAEELRRNLVQPIVVGTGTGIKNSAEEGKNLAPNQQVLILSDKAEVPMYGTWKETAETAE

Query 709 TLAKWLNIELEFQSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 661 TFAKWLNIELEFEGSGSTVQKQDVRANTAIKDIKKIKLTLGD 702
T AKWLNIELEF+GSGSTVQKQDVRANTAIKDIKKI LTLGD

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>dbj|BAD00914.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
dbj|BAD00930.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
dbj|BAD00931.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
dbj|BAD00933.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

```

Score = 1296 bits (3354), Expect = 0.0, Method: Composition-based stats.  
Identities = 662/750 (88%), Positives = 707/750 (94%), Gaps = 0/750 (0%)

```

Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIG+G++FGTDL K 60
MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAVFLVNFAVIIGSGSKFGTDLVK

Query 61 EAKKVHQTRTVPAPKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQ TRTVPAPKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN 120
EAKKVHQITRTVPAPKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFN

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDME+YV+EQLSQPNL QVSFGAKGNGITYANMM+IKKELE AEVKGIDF 180
KVAEVFHKYLDMEAYVKEQLSQPNLTQVSFGAKGNGITYANMMAIKKELETAEVKGIDF

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSMESSLNSILAG DGIITYEKDR 240
TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSMESSLNSILAGKDGIIITYEKDR

Query 241 LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQ+T+DGKDVTYTT+SSPLQSFMETQMDAF EKVKGKMYMTATLVSAKTGE 300
LGNIVPGTEQVSQQTVTDGKDVTYTTLSSPLQSFMETQMDAFLEKVKGKMYMTATLVSAKTGE

Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTF GE FN 360
ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFSGGEYFN

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK 420
SSEFKIADATTRDWDVNDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRFK

Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480
FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI

Query 481 SAIYDPNDQTARKSQKEIVGNPVSQKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVGNPVSQ+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP 540
SAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRNHMILVGTDPVYGTMYNHYTGKPIITVP

Query 541 GQNALVKSQTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNV+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL 600
GQNVAVKSGTAQIADEKNGGYLVGSTNYIFS VVTMNPENPDFILYVTVQQPEHYSGIQL

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP 660
GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQP

Query 661 IVVGTGTGIKNSAEEGKNLAPNQQVLILSDKAEVPMYGTWKETAETLAKWLNIELEF 720
Sbjct 661 IVVGTGTGIK+S EEG NLAPNQQVL+LSDK EE+PDMYGW KETAET AKWL+IELEF 720
IVVGTGTGIKETSVEEGTNLAPNQVLLSLSDKVEEIPDMYGWKETAETFAKWLDIELEF

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750
+GSGS VQKQDVR NTAIK+IKKI LTLGD

```

```

>dbj|BAD00928.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

```


Score = 1294 bits (3348), Expect = 0.0, Method: Composition-based stats.  
Identities = 662/750 (88%), Positives = 706/750 (94%), Gaps = 0/750 (0%)

```

Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

```

Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFA+FLVNFAVIIG+G++FGTDL K MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAVFLVNFAVIIGSGSKFGTDLVK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQ TRTPAKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN	120
Sbjct	61	EAKKVHQITRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF KVAEVFHKYLDME+YV+EQLSQPNL QVSFGAKGNGITYANMM+IKKELE AEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEAYVKEQLSQPNLTQVSFGAKGNGITYANMMAIKKELETAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAG DGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGKDGIIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSATKGE LGNIVPGTEQVSQ+T+DGKDVYTT+SSPLQSFMETQMDAF EKVKGKGYMTATLVSATKGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKDVYTTLSPLQSFMETQMDAFLEKVKGKGYMTATLVSATKGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFN ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVM LA++IDNNTFP GE FN	360
Sbjct	301	ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAFKVMTLASSIDNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK SSE KIADAT RDWDVN GLT G MMTFSQGFAHSSNVG +LLEQKMGDATWLDYL RFK	420
Sbjct	361	SSEFKIADATTRDWDVNAGLTGGRMMTFSQGFAHSSNVGTSLLEQKMGDATWLDYLKRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQKEIVG PVS+DAASLRTNM+LVGTDP+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRKSQKEIVGKPVSEDAASLRTNMILVGTDPVYGTMYNHYTGKPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL GQNV+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEH+SGIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPANPDFILYVTVQQPEHFSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Sbjct	601	GEFATPILERASAMKESLNLQSPAKNLDKVTTESYAMPSIKDISPGELAEALRRNIVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQOVLILSDKAEVDPMYGWTKETATLAKWLNIELEF IVVGTGTKIK +S EEG NLAPNQOVL+LSDK EE+PDYMGW KETAT AKWL+IELEF	720
Sbjct	661	IVVGTGTKIKETSVEEGTNLAPNQOVLILSDKVEEIPDMYGWKKETATFAKWLIDIELEF	720
Query	721	QSGGSTVQKQDVRRANTAIKDIKKITLTLGD 750 +GSGS VQKQDVR NTAIK+IKKI LTLGD	
Sbjct	721	EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750	

>pdb|1PMD|  Chain , Penicillin-Binding Protein 2x (Pbp-2x)  
Length=675

Score = 1294 bits (3348), Expect = 0.0, Method: Composition-based stats.  
Identities = 675/675 (100%), Positives = 675/675 (100%), Gaps = 0/675 (0%)

Query	76	RGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEES RGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEES	135
Sbjct	1	RGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEES	60
Query	136	YVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFAS YVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFAS	195
Sbjct	61	YVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFAS	120
Query	196	SFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRT SFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRT	255
Sbjct	121	SFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRT	180
Query	256	MDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSATKGEILATTQRPTFDADTK MDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSATKGEILATTQRPTFDADTK	315
Sbjct	181	MDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSATKGEILATTQRPTFDADTK	240
Query	316	EGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWD EGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWD	375
Sbjct	241	EGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWD	300
Query	376	VNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAG VNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAG	435
Sbjct	301	VNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAG	360
Query	436	QLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQ QLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQ	495
Sbjct	361	QLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQ	420

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Query 496 KEIVGNPVSFDAASLRTNMLVVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIAD 555
Sbjct 421 KEIVGNPVSFDAASLRTNMLVVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIAD 480

Query 556 EKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK 615
Sbjct 481 EKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK 540

Query 616 DSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAE 675
Sbjct 541 DSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAE 600

Query 676 EGKNLAPNQVVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEFQSGSGSTVQKQDVRAN 735
Sbjct 601 EGKNLAPNQVVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEFQSGSGSTVQKQDVRAN 660

Query 736 TAIKDIKKITLTLGD 750
Sbjct 661 TAIKDIKKITLTLGD 675

```

>gb|AAC45547.1| low-affinity penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1284 bits (3323), Expect = 0.0, Method: Composition-based stats.  
Identities = 654/750 (87%), Positives = 704/750 (93%), Gaps = 0/750 (0%)

```

Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKRITRFAIRNRKSPAENRKIVGKYISLLAVVLFVAVFLVNFAVIIGSGSKFGTDLVK 60

Query 61 EAKKVHQTRTVPKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQITRTVPKRGTIYDRNGVPIAEDATSYNVYAVIDDKYKSATGKILYVEDAQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLQVVSFGAKGNGITANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLQVVSFG+KGNGITANMM+IKKELEAEVKGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR 240

Query 241 LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 VGNIVPGTELVSQQTVDGKDVTYTTLSPLQSFMETQMDAFLEKVKGYMTATLVSAKTGE 300

Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN 360

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK 420

Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPVSFDAASLRTNMLVVGTDVPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVGNPVSK+AAS TR +M+LVGTD+YGTMYNH TGKP +TVP 540

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPENPDFILYVTVQQPEHYSGIQL 600

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP 660

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF 720
Sbjct 661 IVVGTGTKIK+S EEG NLAPNQVVL+LSDK EE+PDYMGW KETAET AKWL+IELEF 720

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750

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>dbj|BAD00915.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1279 bits (3310), Expect = 0.0, Method: Composition-based stats.  
Identities = 651/750 (86%), Positives = 702/750 (93%), Gaps = 0/750 (0%)

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Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKR+ R+A +NRKSPAENR+ VGK +SLL+V +FA+FLVNFAVIIG+G++FGTDL K 60
MKWTKRITRFAIRNRKSPAENRKIVGKYISLLAVVLFAVFLVNFAVIIGSGSKFGTDLVK

Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQ TRTPAKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN 120
EAKKVHQITRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEAYVKEQLSQPNLTQVSFGAKGNGITYANMMAIKKELETAEVKGIDF 180
KVAEVFHKYLDMEAYVKEQLSQPNLTQVSFGAKGNGITYANMMAIKKELETAEVKGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR 240
TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGKDGDIITYEKDR 240

Query 241 LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQ+T+DGKDVYTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGE 300
LGNIVPGTEQVSQQTVDGKDVYTTLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGE 300

Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYEPGSTMKVMMMLAAIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNEYEPS KVMMLA++IDNNTFP GE FN 360
ILATTQRPTFNADTKEGITEDFVWRDILYQSNEYEPGSFAKVMMLASSIDNNTFPSGEYFN 360

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVNEGLT G MMTF SQFAHSSNVGM +LLEQKMGDATWLDYL RFK 420
SSEFKIADATTRDWDVNEGLTTGGMMTFSQGFAHSSNVGTSLLEQKMGDATWLDYLNRFK 420

Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480
FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVGNPVSKEAAS TR +M+LVGTDP+YGTMYNH TGKP +TVP 540
SAIYDTNNQSVRKSQKEIVGNPVSKEAASLRTNMHMLVGTDPVYGTMYNHSTGKPTVTVP 540

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL 600
GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQL 600

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP 660
GEFATPILERASAMKESLNLQSPAKNLKDVTTESYAMPSIKDISPGELAEALRRNLVQP 660

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVPMYGWTKETAETLAKWLNIELEF 720
Sbjct 661 IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PDYMGW KETAET AKWL+IELEF 720
IVVGTGTKIKETSVEEGTNLAPNQVLLLSLSDKVEEIPDYGWKKETAETFAKWLIELEF 720

Query 721 QSGSGTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 +GSGS VQKQDVR NTAIK+IKKI LTLGD 750
EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750

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>dbj|BAD00940.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750

Score = 1275 bits (3300), Expect = 0.0, Method: Composition-based stats.  
Identities = 647/750 (86%), Positives = 702/750 (93%), Gaps = 0/750 (0%)

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Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKR+ R+A +NRKSPAENR+ VGK +SLL+V +FA+FLVNFAVIIG+G++FGTDL K 60
MKWTKRITRFAIRNRKSPAENRKIVGKYISLLAVVLFAVFLVNFAVIIGSGSKFGTDLVK

Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQ TRTPAKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN 120
EAKKVHQITRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEAYVKEQLSQPNLTQVSFGAKGNGITYANMMAIKKDLKDVKEGIDF 180
KVAEVFHKYLDMEAYVKEQLSQPNLTQVSFGAKGNGITYANMMAIKKDLKDVKEGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR 240
TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGKDGDIITYEKDR 240

Query 241 LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQ+T+DGKDVYTT+SSPLQSFME+QMDAFQEK+KGYMTATLVSAKTGE 300
LGNIVPGTEQVSQQTVDGKDVYTTLSSPLQSFMESQMDAFQEKLVKGYMTATLVSAKTGE 300

Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYEPGSTMKVMMMLAAIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYEPS MKVM LA++IDNNTFP GE FN 360
ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYEPGSAMKVMTLASSIDNNTFPSGEYFN 360

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK 420
SSEFKIADATTRDWDVNEGLTTGGMMTFSQGFAHSSNVGMLLEQKMGDATWLDYLNRFK 420

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Sbjct	361	SSEFKIADATTRDWDVNEGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRKFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVAKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLSDKAEVPMYGTWKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK +S EEG NLAPNQVLLSDK EE+PDYMGW KETAET AKWL+IELEF	720
Query	721	QSGSGTVQKQDVRANTAIKDIKKITLTLGD	750
Sbjct	721	EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD	750

>gb|AA56845.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=666

Score = 1271 bits (3290), Expect = 0.0, Method: Composition-based stats.  
Identities = 664/665 (99%), Positives = 664/665 (99%), Gaps = 0/665 (0%)

Query	82	RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL	141
Sbjct	1	RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL	60
Query	142	SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA	201
Sbjct	61	SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA	120
Query	202	QLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV	261
Sbjct	121	QLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV	180
Query	262	YTTISSPLQSFMETQMDAFQEKVKGKYMATLVSAKTGEILATTQRPTFDADTKEGITED	321
Sbjct	181	YTTISSPLQSFMETQMDAFQEKVKGKYMATLVSAKTGEILATTQRPTFDADTKEGITED	240
Query	322	FVWRDILYQSNEYEPGSTMKVMLAAAIIDNNTFPGGEVFNSSELKIADATIRDWDVNEGLT	381
Sbjct	241	FVWRDILYQSNEYEPGSTMKVMTLAAAIIDNNTFPGGEVFNSSELKIADATIRDWDVNEGLT	300
Query	382	GGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN	441
Sbjct	301	GGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN	360
Query	442	IVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN	501
Sbjct	361	IVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN	420
Query	502	PVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGY	561
Sbjct	421	PVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGY	480
Query	562	LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ	621
Sbjct	481	LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ	540
Query	622	TTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA	681
Sbjct	541	TTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA	600
Query	682	PNQQVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGTVQKQDVRANTAIKDI	741
Sbjct	601	PNQQVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGTVQKQDVRANTAIKDI	660
Query	742	KKITL	746
Sbjct	661	KKITL	665

>dbj|BAD00908.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
>dbj|BAD00911.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=750



Score = 1269 bits (3283), Expect = 0.0, Method: Composition-based stats.  
Identities = 643/750 (85%), Positives = 696/750 (92%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSAPENRRRVGKSLSLLSVVFVFAIFLVNFAVIGTGRFGTDLAK	60
Sbjct	1	MKWT+++ R+A KNRKSPA+NRR VGK LS ++V +FA+FL NFA II G FGTDL K	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEAYVKEQLAQPNLTQVSFGAKNGGITYANMMAIKNDLKTAGVEGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDG+K L+G+SG+ESSLSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQ SQ T+DGKDVYTT+SSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTF+ADTK+GIT+DFVWRDILYQSNYEPGS MKVM LA+AIDNNTFPGGE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVN+GLT G MMTFSQGFHSSNVGM+LLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEY GQLPADNIVNIA S+FGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTV	540
Sbjct	481	SAIYDPNDQ+ RKSQKEIVGNPVSK AAS TR +MV+VGTDPVYGTMYNHSTGKPVNV	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYL G T+YIFS VSM PAENPDFILYVTVQQPEHYSGL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVPMYGTWKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK SS EEG NLAPNQVLL+LSDK EE+PDYMGW KETAET AKWL+IELEF	720
Query	721	QSGSGTVQKQDVRANTAIKDIKITLTLGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	

>gb|ABB46504.1| penicillin binding protein 2x [Streptococcus pneumoniae]  
gb|ABB46507.1| penicillin binding protein 2x [Streptococcus pneumoniae]  
Length=657

Score = 1258 bits (3254), Expect = 0.0, Method: Composition-based stats.  
Identities = 656/657 (99%), Positives = 657/657 (100%), Gaps = 0/657 (0%)

Query	94	YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGA	153
Sbjct	1	YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGA	60
Query	154	KNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSL	213
Sbjct	61	KNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSL	120
Query	214	LGTSGMESSLSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPLQSF	273
Sbjct	121	LGTSGMESSLSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPLQSF	180
Query	274	ETQMDAFQEKVKGKMYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNY	333
Sbjct	181	ETQMDAFQEKVKGKMYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNY	240
Query	334	EPGSTMKVMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFA	393
Sbjct	241	EPGSTMKVMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFA	300
Query	394	HSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG	453
Sbjct	301	HSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG	360

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Query   454   ISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAASLTRT   513
Sbjct   361   ISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAASLTRT   420

Query   514   NMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV   573
Sbjct   421   NMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV   480

Query   574   SMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQ   633
Sbjct   481   SMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQ   540

Query   634   SPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTIKNSSAEEGKNLAPNQVVLILSDKA   693
Sbjct   541   SPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTIKNSSAEEGKNLAPNQVVLILSDKA   600

Query   694   EEVPDMPYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLGD   750
Sbjct   601   EEVPDMPYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLGD   657

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>gb|AAN32862.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=661

Score = 1235 bits (3195), Expect = 0.0, Method: Composition-based stats.  
Identities = 643/661 (97%), Positives = 652/661 (98%), Gaps = 0/661 (0%)

```

Query   90   DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV   149
Sbjct   1    DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV   60

Query   150   SFGAKGNGITYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG   209
Sbjct   61   SFG+KGNGITYANMMSIKKELE AEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG   120

Query   210   SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPL   269
Sbjct   121  SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTTISSPL   180

Query   270   QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY   329
Sbjct   181  QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGIT+DFVWRDILY   240

Query   330   QSNYEPGSTMTKMVMLAAAI DNNTFPGGEVFNSELKIADATIRDWDVNEGLTGGRMMTFS   389
Sbjct   241  QSNYEPGSAMKVMTLAAAI DNNTFPGGEVFNSELKVADVTTTRDWDVNEGLTGGMMTFS   300

Query   390   QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS   449
Sbjct   301  QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS   360

Query   450   FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAAS   509
Sbjct   361  FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKE+VGNPVSKDAAS   420

Query   510   LTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYI   569
Sbjct   421  LTRTHMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTNYI   480

Query   570   FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ   629
Sbjct   481  FSAVSM+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ   540

Query   630   VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTIKNSSAEEGKNLAPNQVVLIL   689
Sbjct   541  VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTIKNSSAEEGKNLAPNQVVLIL   600

Query   690   SDKAEVDPDMPYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLG   749
Sbjct   601  SDKAEVDPDMPYGTWKATAETFAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLG   660

Query   750   D      750
Sbjct   661   D      661

```

>gb|AAN32857.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
>gb|AAN32858.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=661

Score = 1234 bits (3194), Expect = 0.0, Method: Composition-based stats.  
Identities = 643/661 (97%), Positives = 653/661 (98%), Gaps = 0/661 (0%)

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Query   90   DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV   149
Sbjct   1    DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV

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Sbjct	1	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKGNGITIYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG	209
Sbjct	61	SFGAKGNGITIYANMMSIKKELEAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPL	269
Sbjct	121	SKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQ+SQ+T+DGKDVYTTISSPL	180
Query	270	QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	329
Sbjct	181	QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGIT+DFVWRDILY	240
Query	330	QSNYEPGSTMKVMMLAAAI DNNTFPGGEVFNSSSELKIADATIRDWVDVNEGLTGGRMMTFS	389
Sbjct	241	QSNYEPGS MKVM LAA+IDNNTFPGGE FNSSELKIAD TIRDWVDVNEGLTGG MMTFS	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	360
Query	450	FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS	509
Sbjct	361	FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS	420
Query	510	LTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYI	569
Sbjct	421	LTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLT+YI	480
Query	570	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
Sbjct	481	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAK+LEQ	540
Query	630	VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGVTGTKIKNSSAEEGKNLAPNQVVLIL	689
Sbjct	541	VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGVTGTKIKNSSAEEGKNLAPNQVVLIL	600
Query	690	SDKAEVDPDYGWTKETAETLAKWLNIELEFQSGSGTVQKQDVRANTAIKDIKKITLTLG	749
Sbjct	601	SDKAEVDPDYGWTK TAET AKWLNIELEF+GSG+TVQKQDVRANTAIKDIKKITLTLG	660
Query	750	D 750	
Sbjct	661	D 661	

>emb|CAB65447.1| penicillin binding protein 2x [Streptococcus pneumoniae]  
Length=666

Score = 1230 bits (3182), Expect = 0.0; Method: Composition-based stats.  
Identities = 639/666 (95%), Positives = 653/666 (98%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITIYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITIYANMMSIKKELEAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFW	324
Sbjct	181	ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFW	240
Query	325	RDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFNSSSELKIADATIRDWVDVNEGLTGGR	384
Sbjct	241	RDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFNSSSELKIADATIRDWVDVNEGLTGGR	300
Query	385	MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IA S+FGQGISVTQTQM+RAFTAIANDGVMLEPKFISA+YDPNDQ+ RKSQKEIVGNPVS	420
Query	505	KDAASLTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	K+AAS+TR +MV+VGTD P YGTMYNHSTGK TV VPGQNVALKSGTA+IADEKNGGYL G	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA	624

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-      T+ IFS VSM PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQTTA
Sbjct  481 STNNIFSVMHPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQTTA 540

Query  625 KALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTTIKNSSAEEGKNLAPNQ 684
-      KALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTTIKNSSAEEGKNLAPNQ
Sbjct  541 KALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTTIKNSSAEEGKNLAPNQ 600

Query  685 QVLILSDKAAEVPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI 744
-      QVLILSDKAAEVPDMYGWTKETAET AKWLNIELEF+GSGSTVQKQDVRANTAIKDIKKI
Sbjct  601 QVLILSDKAAEVPDMYGWTKETAETFAKWLNIELEFEGSGSTVQKQDVRANTAIKDIKKI 660

Query  745 TLTLGD 750
-      TLTLGD
Sbjct  661 TLTLGD 666

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>gb|AAN32865.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=661

Score = 1222 bits (3161), Expect = 0.0, Method: Composition-based stats.  
Identities = 636/661 (96%), Positives = 651/661 (98%), Gaps = 0/661 (0%)

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Query  90 DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV 149
Sbjct  1 DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV 60

Query  150 SFGAKGNGITYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG 209
Sbjct  61 SFGAKGNGITYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG 120

Query  210 SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPL 269
Sbjct  121 SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPL 180

Query  270 QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY 329
Sbjct  181 QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITKDFVWRDILY 240

Query  330 QSNYEPGSTMKVMMLAAAI DNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFS 389
Sbjct  241 QSNYEPGSTMKVMMLAAAI DNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGG MMTFS 300

Query  390 QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS 449
Sbjct  301 QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS 360

Query  450 FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS 509
Sbjct  361 FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKE+VGNPVS KDAAS 420

Query  510 LTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYI 569
Sbjct  421 LTRTNMILVGTDPVYGTMYNHSTGKPTVNVPGQNVALKSGTAEIADEKNGGYLVGSTNNI 480

Query  570 FSAVMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ 629
Sbjct  481 FS V+M+PAE+PDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ AK L++ FSVVAMNPAEDPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPAKNLDK 540

Query  630 VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTTIKNSSAEEGKNLAPNQVVLIL 689
Sbjct  541 VTTESSYAMPSIKDISPGDLAEELRRNLVQPIVVGTGTTIKNSSAEEGKNLAPNQVVLIL 600

Query  690 SDKAAEVPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLG 749
Sbjct  601 SDKAAEVPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLG 660

Query  750 D 750
-      D
Sbjct  661 D 661

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>emb|CAD90770.1| penicillin-binding protein 2x [Streptococcus pneumoniae]  
Length=702

Score = 1217 bits (3150), Expect = 0.0, Method: Composition-based stats.  
Identities = 627/702 (89%), Positives = 665/702 (94%), Gaps = 0/702 (0%)

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Query  49 GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 108
Sbjct  1 GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 60

Query  109 GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVVSFGAKGNGITYANMMSIKK 168
Sbjct  61 GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVVSFG+KNGITYANMMSIKK 120

Query  169 ELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 228

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-   Sbjct  121  ELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 180
      ELETAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA

-   Query  229  GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKY 288
      GTDGIITYEKDR+GNIVPGTE VSQ+T+DGKDVTYTT+SSPLQSFMETQMDAF EKVKGKY
-   Sbjct  181  GTDGIITYEKDRVGNIVPGTELVSQQTVDGKDVTYTTLSPLQSFMETQMDAFLEKVKGKY 240

      Query  289  MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI 348
      MTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++I
      Sbjct  241  MTATLVSAKTGEILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSI 300

      Query  349  DNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG 408
      DNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMG
      Sbjct  301  DNNTFPSGEYFNSSEFKIADATT RDWDVNDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMG 360

      Query  409  DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAI 468
      DATWLDYL RKFVGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAI
      Sbjct  361  DATWLDYLRKFKFGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAI 420

      Query  469  ANDGVMLEPKFISAIYDPNDQTARKSKEIVGNPVS KDAASLTRTNMVLVGTDPVYGTMY 528
      ANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTDP+YGTMY
      Sbjct  421  ANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRNHHMILVGTDPPLYGTMY 480

      Query  529  NHSTGKPTVTVPQGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT 588
      NH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVT
      Sbjct  481  NHYTGKPIITVPQGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVT 540

      Query  589  VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGD 648
      VQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+
      Sbjct  541  VQQPEHYSGIQLGEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGE 600

      Query  649  LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEVPMYGTWKETAE 708
      LAE LRRN+VQPIVVGTGTKIK +S EEG NLAPNQQVL+LSDK EE+PMYGTWKETAE
      Sbjct  601  LAEALRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQQVLLLSDKVEEIPMYGWWKETAE 660

      Query  709  TLAKWLNIELEFQGS GSTVQKQDVRANTAIAKDIKKITLTLGD 750
      T AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTLGD
      Sbjct  661  TFAKWL DIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 702

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>emb|CAD90771.2| penicillin-binding protein 2x [Streptococcus pneumoniae]  
Length=702

Score = 1209 bits (3129), Expect = 0.0, Method: Composition-based stats.  
Identities = 622/702 (88%), Positives = 662/702 (94%), Gaps = 0/702 (0%)

```

Query  49  GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 108
      GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT
Sbjct  1  GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 60

Query  109  GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKK 168
      GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMM+IKK
Sbjct  61  GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMAIKK 120

Query  169  ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 228
      +L+ A V+GIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA
Sbjct  121  DLKDAVSEGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 180

Query  229  GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKY 288
      G DGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVTYTT+SSPLQSFMETQMDAF EKVKGKY
Sbjct  181  GKDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVTYTTLSPLQSFMETQMDAFLEKVKGKY 240

Query  289  MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI 348
      MTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVMMLA++I
Sbjct  241  MTATLVSAKTGEILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSFAKVMMLASSI 300

Query  349  DNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG 408
      DNNTFP GE FNSSE KIADAT RDWDVN GLT G MMTF QGFAHSSNVG +LLEQKMG
Sbjct  301  DNNTFPSGEYFNSSEFKIADATT RDWDVNAGLTTGGMMTFLQGFAHSSNVGTSLLEQKMG 360

Query  409  DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAI 468
      DATWLDYL RKFVGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAI
Sbjct  361  DATWLDYLRKFKFGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAI 420

Query  469  ANDGVMLEPKFISAIYDPNDQTARKSKEIVGNPVS KDAASLTRTNMVLVGTDPVYGTMY 528
      ANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTDP+YGTMY
Sbjct  421  ANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRNHHMILVGTDPPLYGTMY 480

Query  529  NHSTGKPTVTVPQGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT 588
      NH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVT
Sbjct  481  NHYTGKPIITVPQGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVT 540

Query  589  VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGD 648
      VQQPEH+SGIQLGEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+
Sbjct  541  VQQPEHFSGIQLGEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGE 600

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- Query 649 LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPMDYGWTKETAE 708
  Sbjct 601 LAE LRRN+VQPIVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PMDYGW KETAE 660
  LAELRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQVLLILSDKVVEEIPMDYGWKKETAE

- Query 709 TLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
  Sbjct 661 T AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTLGD 702
  TFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTLGD

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>gb|AA556843.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
 gb|AA556844.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
 Length=669

Score = 1207 bits (3122), Expect = 0.0, Method: Composition-based stats.  
 Identities = 625/669 (93%), Positives = 648/669 (96%), Gaps = 0/669 (0%)

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Query 82  RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL 141
Sbjct 1  RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL 60

Query 142 SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA 201
Sbjct 61 SQPNLKQVSFG+KNGGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLA 120
SQPNLKQVSFGSKGNGITYANMMSIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGLA

Query 202 QLHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDV 261
Sbjct 121 QLHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQ+T+DGKDV 180
QLHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQQTVDGKDV

Query 262 YTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITED 321
Sbjct 181 YTTISSPLQSFMETQMDAF +KVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITED 240
YTTISSPLQSFMETQMDAF LQKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITED

Query 322 FVWRDILYQSNEYEPGSTMKVMMLAAAI DNNTFPGGEVFNSSELKIADATIRDWDVNEGLT 381
Sbjct 241 FVWRDILYQSNEYEPGS +KVM LA++IDNNTFP GE FNSSE KIAD T RDWDVN+GLT 300
FVWRDILYQSNEYEPGSALKVMTLASSIDNNTFPSGEYFNSSEFKIADVTRDWDVNDGLT

Query 382 GGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN 441
Sbjct 301 G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN 360
TGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN

Query 442 IVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQQEIVGN 501
Sbjct 361 IVNIAQSSFGQGISVTQTQM+RA TAIANDGVMLEPKFISAIYD N+Q+ RKSQQEIVG 420
IVNIAQSSFGQGISVTQTQMLRALTAIANDGVMLEPKFISAIYDTNNQSVRKSQQEIVGK

Query 502 PVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGY 561
Sbjct 421 PVS+DAASLTRTNM+LVGTDP+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGY 480
PVSEDAASLTRTNMILVGTDP IYGTMYNHYTGKPIITVPGQNVAVKSGTAQIADEKNGGY

Query 562 LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ 621
Sbjct 481 LVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ 540
LVGSTNYIFSVVTMNPANPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQ

Query 622 TTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA 681
Sbjct 541 TTAKALEQVS+QSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA 600
TTAKALEQVSKQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA

Query 682 PNQQVLLILSDKAEVDPMDYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDI 741
Sbjct 601 PNQQVLLILSDKAEVDPMDYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDI 660
PNQQVLLILSDKAEVDPMDYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDI

Query 742 KKITLTLGD 750
Sbjct 661 KKITLTLGD 669

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>gb|AA556850.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
 Length=670

Score = 1206 bits (3119), Expect = 0.0, Method: Composition-based stats.  
 Identities = 627/670 (93%), Positives = 647/670 (96%), Gaps = 0/670 (0%)

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Query 81  DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ 140
Sbjct 1  DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ 60
DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ

Query 141 LSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGL 200
Sbjct 61 LSQPNLKQVSFGAKGNGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGL 120
LSQPNLKQVSFGAKGNGITYANMMSIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGL

Query 201 AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKD 260
Sbjct 121 AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQ+T+DGKD 180
AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQQTVDGKD

Query 261 VYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITE 320
Sbjct 181 VYTTISS LQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITE 240
VYTTISS TLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITE

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Query 321 DFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFP GGGEVFNSSSELKIADATIRDWDVNEGL 380
Sbjct 241 DFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GL 300

Query 381 TGGRRMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPAD 440
Sbjct 301 TGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFKFGVPTRFGLTDEYAGQLPAD 360

Query 441 NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVG 500
Sbjct 361 NIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVG 420

Query 501 NPVSKDAASLTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGG 560
Sbjct 421 NPVSKEAASSTRNHMILVGTDPLYGTMYNHSTGKPIITVPQGNVAVKSGTAQIADEKNGG 480

Query 561 YLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL 620
Sbjct 481 YLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKDSLNL 540

Query 621 QTTAKALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNL 680
Sbjct 541 QTTAKALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNL 600

Query 681 APNQQVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQGGSGSTVQKQDVRANTAIKD 740
Sbjct 601 APNQQVLILSDKVEEVPDMYGTWKETAETLAKWLNIELEFQGGSGSTVQKQDVRANTAIKD 660

Query 741 IKKITLTLGD 750
Sbjct 661 IKKITLTLGD 670

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>gb|AA556847.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=669

Score = 1204 bits (3114), Expect = 0.0, Method: Composition-based stats.  
Identities = 621/669 (92%), Positives = 644/669 (96%), Gaps = 0/669 (0%)

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Query 82 RNVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL 141
Sbjct 1 RNVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL 60

Query 142 SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA 201
Sbjct 61 SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA 120

Query 202 QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV 261
Sbjct 121 QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV 180

Query 262 YTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITED 321
Sbjct 181 YTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITED 240

Query 322 FVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFP GGGEVFNSSSELKIADATIRDWDVNEGLT 381
Sbjct 241 FVWRDILYQSNYEPGSTMKVM LAAAI DNNTFP GGGEVFNSSSELKIADATIRDWDVNEGLT 300

Query 382 GGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN 441
Sbjct 301 GGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN 360

Query 442 IVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN 501
Sbjct 361 IVNIA S+FGQGISVTQTQM+RAFTAIANDGVMLEPKFISA+YDPNDQ+ RKSQKE+VGN 420

Query 502 PVSCKDAASLTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGGY 561
Sbjct 421 PVSKEAASVTRDQMVMVGTDPTYGTMYNHSTGKATVNVPGQGNVALKSGTAEIADEKNGGY 480

Query 562 LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ 621
Sbjct 481 LVGSTNNIFSVVAMNPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ 540

Query 622 TTAKALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA 681
Sbjct 541 SPAKNLDQVTTESYAMPSIKDISPGDLAEALRRNIVQPIVVGTGTKIKESSVEEGKNLA 600

Query 682 PNQQVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQGGSGSTVQKQDVRANTAIKDI 741
Sbjct 601 PNQQVLLLSDKVEEIPDMYGWKKETAETFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNI 660

Query 742 KKITLTLGD 750
Sbjct KKI LTLGD

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- Sbjct 661 KKIKLTLGD 669

>gb|AA556846.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=670

Score = 1198 bits (3099), Expect = 0.0, Method: Composition-based stats.  
Identities = 621/670 (92%), Positives = 647/670 (96%), Gaps = 0/670 (0%)

Query	81	DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ	140
Sbjct	1	DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ	60
Query	141	LSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKIGIDFTTSPNRSYPNGQFASSFIGL	200
Sbjct	61	LSQPNLKQVSFGAKGNGITYANMMAIKKELETAEVKIGIDFTTSPNRSYPNGQFASSFIGL	120
Query	201	AQLHENEDGSKSLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKD	260
Sbjct	121	AQLHENEDGSKSLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQ+T+DGKD	180
Query	261	VYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITE	320
Sbjct	181	VYTTISS LQSFMETQM+AFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEG+T+	240
Query	321	DFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWVDNEGL	380
Sbjct	241	DFVWRDILYQSNYEPGSTMKVM LAAIDNNTFPGGEVFNSSSELK+AD TIRDWVDNEGL	300
Query	381	TGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPAD	440
Sbjct	301	TGG MMTFSQGF A SSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPAD	360
Query	441	NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVG	500
Sbjct	361	NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISA+YDPNDQ+ RKSQKEIVG	420
Query	501	NPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGG	560
Sbjct	421	NPVSK+AAS+TR +MV+VGTD YGTMYNHSTGKPTVTVPQGNVALKSGTA+IADEKNGG	480
Query	561	YLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL	620
Sbjct	481	YLVG T+YIFSAVSM+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNL	540
Query	621	QTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGKTIKNSSAEEGKNL	680
Sbjct	541	Q+TAK LEQ S+ + Y MP+ KD +PGDLAEELRRNLVQPIVVGTGKTIK +S EEG NL	600
Query	681	APNQVLLILSDKAEEVPDYGWTKETAETLAKWLNIELEFGSGSTVQKQDVRANTAIKD	740
Sbjct	601	APNQVLL+LSDK EE+PDYGW KETAET AKWLNIELEF+GSGSTVQKQDVRANTAIKD	660
Query	741	IKKITLTLGD 750	
Sbjct	661	IKKITLTLGD 670	

>gb|AA556857.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=666

Score = 1197 bits (3096), Expect = 0.0, Method: Composition-based stats.  
Identities = 623/666 (93%), Positives = 643/666 (96%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITYANMMSIKKELETAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTT	264
Sbjct	121	ENEDGSKSLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQ+T+DGKDVTYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	ISS LQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVW	240
Query	325	RDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWVDNEGLTGGR	384
Sbjct	241	RDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G	300
Query	385	MMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444
		MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RKFVGVPTRFGLTDEYAGQLPADNIV+	



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* Sbjct 301 MMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFKFGVPTRFGLTDEYAGQLPADNIVS 360
Query 445 IAQSSFGQGIGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS 504
IAQSSFGQGIGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS
* Sbjct 361 IAQSSFGQGIGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVS 420
Query 505 KDAASLRTNMLVLTGDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVG 564
K+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVPGQNV+A+KSGTAQIADEKNGGYLVG
Sbjct 421 KEAASLRTNMLVLTGDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVG 480
Query 565 LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQLGEFANPILERASAMKDSLNLQTTA 624
T+YIFS V+M+PAENPDFILYVTVQQPEHYSIGIQLGEFA PILERASAMKDSLNLQTTA
Sbjct 481 STNYIFSVMNPAENPDFILYVTVQQPEHYSIGIQLGEFATPILERASAMKDSLNLQTTA 540
Query 625 KALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQ 684
KALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQ
Sbjct 541 KALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQ 600
Query 685 QVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI 744
QVLILSDK EEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI
Sbjct 601 QVLILSDKVEEVPDMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI 660
Query 745 TLTLGD 750
Sbjct 661 TLTLGD 666

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>emb|CAB65444.1| penicillin binding protein 2x [Streptococcus pneumoniae]  
Length=666

Score = 1188 bits (3073), Expect = 0.0, Method: Composition-based stats.  
Identities = 612/666 (91%), Positives = 640/666 (96%), Gaps = 0/666 (0%)

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Query 85 VPAAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 144
Sbjct 1 VPAAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 60
Query 145 NLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH 204
NLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH
Sbjct 61 NLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH 120
Query 205 ENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT 264
ENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT
Sbjct 121 ENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT 180
Query 265 ISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW 324
+SSPLQSFMETQMDAF +KVKGYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVW
Sbjct 181 LSSPLQSFMETQMDAFLQKVKGYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFVW 240
Query 325 RDILYQSNYEPGSTMKVMMMLAAAI DNNTFPGGGEVFNSELKIADATIRDWDVNEGLTGGR 384
RDILYQSNYEPGS MKVM LAAAI DNNTFPGGE FNSSELKIAD TIRDWDVN+GLT GR
Sbjct 241 RDILYQSNYEPGSAMKVMMLAAAI DNNTFPGGGEVFNSELKIADVTIRDWDVNDGLTTGR 300
Query 385 MMTFSQGFHSSNVGMSLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN 444
MMTF QGFA SSVNGM+LLEQKMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN
Sbjct 301 MMTFLQGFALSSNVGMSLLEQKMGDPWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN 360
Query 445 IAQSSFGQGIGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS 504
IAQSSFGQGIGISVTQTQMIRAFTAIANDGVMLEPKFI+A+YDPNDQT RKSQKEIVGNPVS
Sbjct 361 IAQSSFGQGIGISVTQTQMIRAFTAIANDGVMLEPKFITALYDPNDQTVRKSQKEIVGNPVS 420
Query 505 KDAASLRTNMLVLTGDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVG 564
KDAASLRTNM+LVGTDPVYGTMYNHSTGKPTVTVPQNVALKSGTA+IADEKNGGYLVG
Sbjct 421 KDAASLRTNMILVLTGDPVYGTMYNHSTGKPTVTVPQNVALKSGTAETIADEKNGGYLVG 480
Query 565 LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQLGEFANPILERASAMKDSLNLQTTA 624
T+YIFS V+M+PAENPDFILYVTVQQPEHYSIGIQLGEFANPILERASAMK+SLNLQ+ A
Sbjct 481 STNYIFSVMNPAENPDFILYVTVQQPEHYSIGIQLGEFANPILERASAMKESLNLQSPA 540
Query 625 KALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQ 684
K L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTGIK +S EEGKNLAPNQ
Sbjct 541 KNLDQVTTESSYAMPSIKDISPGELAEELRRNIVQPIVVGTGTGIKETSVEEGKNLAPNQ 600
Query 685 QVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI 744
QVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI
Sbjct 601 QVLLLSDKVEEIPDMYGWKKETAETFAKWLDIELEFEGSGSIVQKQDVRTNTAIKNIKKI 660
Query 745 TLTLGD 750
Sbjct 661 KTLTGD 666

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>gb|AAN32852.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
 gb|AAN32853.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
 gb|AAN32854.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
 Length=661

Score = 1187 bits (3071), Expect = 0.0, Method: Composition-based stats.  
Identities = 618/661 (93%), Positives = 638/661 (96%), Gaps = 0/661 (0%)

Query	90	DATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV	149
Sbjct	1	DATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKGNGITYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG	209
Sbjct	61	SFGAKGNGITYANMMSIKKELE AEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPL	269
Sbjct	121	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTTISS L	180
Query	270	QSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	329
Sbjct	181	QSFMETQMDAF EKVKGKGYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILY	240
Query	330	QSNYEPGSTMKVMMLAAAI DNNTFP GGEVFNSSSELKIADATIRDWVDVNEGLTGGRMMTFS	389
Sbjct	241	QSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSS	360
Query	450	FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS	509
Sbjct	361	FGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS K+AAS	420
Query	510	LTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYI	569
Sbjct	421	TR +M+LVGTD+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG T+YI	480
Query	570	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
Sbjct	481	FS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMKDSLNLQTTAKALEQ	540
Query	630	VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGVTGTKIKNSSAEEGKNLAPNQVVLIL	689
Sbjct	541	VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGVTGTKIKNSSAEEGKNLAPNQVVLIL	600
Query	690	SDKAEVDPDMPYGTWKETAETLAKWLNIELEFQGSSTVQKQDVRANTAIKDIKKITLTLG	749
Sbjct	601	SDK EEVDPDMPYGTWKETAETLAKWLNIELEFQGSSTVQKQDVRANTAIKDIKKITLTLG	660
Query	750	D 750	
Sbjct	661	D 661	

>gb|AAN32861.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=661

Score = 1186 bits (3069), Expect = 0.0, Method: Composition-based stats.  
Identities = 614/661 (92%), Positives = 635/661 (96%), Gaps = 0/661 (0%)

Query	90	DATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV	149
Sbjct	1	DATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKGNGITYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG	209
Sbjct	61	SFGAKGNGITYANMMSIKKELE AEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPL	269
Sbjct	121	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTTISS L	180
Query	270	QSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	329
Sbjct	181	QSFMETQM+AFQEKVKGYMTA LVSAKTGEILATTQRPTFDADTKEG+T+DFVWRDILY	240
Query	330	QSNYEPGSTMKVMMLAAAI DNNTFP GGEVFNSSSELKIADATIRDWVDVNEGLTGGRMMTFS	389
Sbjct	241	QSNYEPGS MKVM LAAAI DNNTFP GGEVFNSSSELK+AD TIRDWDVNEGLTG MMTFS	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	360
Query	450	FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS	509
Sbjct	361	FGQGISVTQTQMIRAFTAIANDGVMLEPKFISA+YDPNDQT RKSQKEIVGNPVS KDAAS	420

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Query   510  LTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYI  569
Sbjct   421  QTRTHMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGTTDYI  480

Query   570  FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ  629
Sbjct   481  FSAVSM+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERA AMKDSLNLQ+TAK L+Q  540
FSAVSMNPAENPDFILYVTVQQPEHYSGIQLGEFANPILERAVAMKDSLNLQSTAKTLDQ

Query   630  VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLIL  689
Sbjct   541  VTNQSAYAMPSIKDISPGDLAEALRRNIVQPIVVGTGTKIKESSVEEGTNLAPNQVILL  600

Query   690  SDKAEVVPDMPYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTG  749
Sbjct   601  SDK EE+PDMPYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTG  660
SDKVEEIPDMPYGWKKETAETFAKWL DIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTG

Query   750  D 750
Sbjct   661  D 661

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>gb|AAN32863.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=661

Score = 1183 bits (3061), Expect = 0.0, Method: Composition-based stats.  
Identities = 611/661 (92%), Positives = 639/661 (96%), Gaps = 0/661 (0%)

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Query   90  DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV  149
Sbjct   1  DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV  60

Query   150  SFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG  209
Sbjct   61  SFG+KNGNGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG  120
SFGSKGNGITYANMMSIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG

Query   210  SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPL  269
Sbjct   121  SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTTISSPL  180
SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVYTTISSPL

Query   270  QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY  329
Sbjct   181  QSFMETQ+AFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEG+T+DFVWRDILY  240
QSFMETQMNAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGLTADFVWRDILY

Query   330  QSNYEPGSTMKVMMLAAAI DNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGRMMTFS  389
Sbjct   241  QSNYEPGSTMKVM LAAAI DNNTFPGGEVFNSSELKIAD TIRDWDVN+GLT GRMMTF  300
QSNYEPGSTMKVMTLAAAI DNNTFPGGEVFNSSELKIADV TIRDWDVNDGLTTGRMMTFL

Query   390  QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS  449
Sbjct   301  QGFALSSNVGMSLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS  360
QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS

Query   450  FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS  509
Sbjct   361  FGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKE+VGNPVS KDAAS  420
FGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEVVGNPVS KDAAS

Query   510  LTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYI  569
Sbjct   421  LTRTNM+LVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLT+YI  480
LTRTNMILVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTNYI


Query   570  FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ  629
Sbjct   481  FSAVSM+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ AK L++  540
FSAVSMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPAKNLDK


Query   630  VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLIL  689
Sbjct   541  VTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQVLLL  600


Query   690  SDKAEVVPDMPYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTG  749
Sbjct   601  SDK EE+PDMPYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTG  660
SDKVEEIPDMPYGWKKETAETFAKWL DIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTG

Query   750  D 750
Sbjct   661  D 661

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>pdb|1K25|A  Chain A, Pbp2x From A Highly Penicillin-Resistant Streptococcus pneumoniae Clinical Isolate

>pdb|1K25|B  Chain B, Pbp2x From A Highly Penicillin-Resistant Streptococcus pneumoniae Clinical Isolate

>pdb|1K25|C  Chain C, Pbp2x From A Highly Penicillin-Resistant Streptococcus pneumoniae Clinical Isolate

pdb|1K25|D Chain D, Pbp2x From A Highly Penicillin-Resistant Streptococcus  
Pneumoniae Clinical Isolate  
Length=685

Score = 1183 bits (3060), Expect = 0.0, Method: Composition-based stats.  
Identities = 607/685 (88%), Positives = 646/685 (94%), Gaps = 0/685 (0%)

Query	66	HQTRTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEV	125
Sbjct	1	HQ TRTVP AKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFNKVAEV	60
Query	126	FHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDFTTSPN	185
Sbjct	61	FHKYLDMEESYVREQLSQPNLKQVSFG+KNGITYANMM+IKKELE AEVKGIDFTTSPN	120
Query	186	RSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIV	245
Sbjct	121	RSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR+GNIV	180
Query	246	PGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGEILATT	305
Sbjct	181	PGTE VSQ+T+DGKDVYTT+SSPLQSFMETQMDAF EKVKGKMYMTATLVSAKTGEILATT	240
Query	306	QRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFP GGGEVFNSSSELK	365
Sbjct	241	QRPTFNADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSELK	300
Query	366	IADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPT	425
Sbjct	301	IADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPT	360
Query	426	RFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYD	485
Sbjct	361	RFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD	420
Query	486	PNDQTARKSQKEIVGNPVS KDAASL TRTNMVLVGTDPVYGTMYNHSTGKPTVTVPGQNVA	545
Sbjct	421	N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNVA	480
Query	546	LKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFAN	605
Sbjct	481	+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQLGEFA	540
Query	606	PILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVGT	665
Sbjct	541	PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVGT	600
Query	666	GTKIKNSSAEEGKNLAPNQVLLISDKAEEVPDMYGWTKETAETLAKWLNIELEFQSGSGS	725
Sbjct	601	GTKIK +S EEG NLAPNQVLL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS	660
Query	726	TVQKQDVRANTAIDIKKITLTLGD	750
Sbjct	661	VQKQDVR NTAIK+IKKI LTLGD	685

>gb|ABB46505.1| penicillin binding protein 2x [Streptococcus pneumoniae]  
Length=657

Score = 1182 bits (3059), Expect = 0.0, Method: Composition-based stats.  
Identities = 614/657 (93%), Positives = 635/657 (96%), Gaps = 0/657 (0%)

Query	94	YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGA	153
Sbjct	1	YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGA	60
Query	154	KNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSL	213
Sbjct	61	KNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSL	120
Query	214	LGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSF	273
Sbjct	121	LGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTTISS LQSF	180
Query	274	ETQMDAFQEKVKGKMYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNY	333
Sbjct	181	ETQMDAF EKVKGKMYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILYQSNY	240
Query	334	EPGSTMKVMMLAAAI DNNTFP GGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGF	393
Sbjct	241	EPGS MKVM LA+++DNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF QGFA	300
Query	394	HSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG	453
Sbjct	301	HSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQG	360

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Query   454   ISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSFDAASLTRT   513
Sbjct   361   ISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRN   420

Query   514   NMVLVGTDVPYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV   573
Sbjct   421   HMILVGTDPLYGTMYNHSTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVV   480

Query   574   SMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQ   633
Sbjct   481   TMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKDSLNLQTTAKALEQVSQQ   540

Query   634   SPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKA   693
Sbjct   541   SPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKV   600

Query   694   EEVPDAMYGWTKEATAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLGD   750
Sbjct   601   EEVPDAMYGWTKEATAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLGD   657

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>gb|ABB46506.1| penicillin binding protein 2x [Streptococcus pneumoniae]  
Length=657

Score = 1181 bits (3055), Expect = 0.0, Method: Composition-based stats.  
Identities = 614/657 (93%), Positives = 634/657 (96%), Gaps = 0/657 (0%)

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Query   94   YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGA   153
Sbjct   1     YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGA   60

Query   154   KNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSL   213
Sbjct   61   KNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSL   120

Query   214   LGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSF   273
Sbjct   121   LGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSF   180

Query   274   ETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNY   333
Sbjct   181   ETQMDAFLEKVKGYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFVWRDILYQSNY   240

Query   334   EPGSTMKVMMLAAIDNNTFFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGF   393
Sbjct   241   EPGSAMKVMMLTASSIDNNTFFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFLQGF   300

Query   394   HSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG   453
Sbjct   301   HSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG   360

Query   454   ISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSFDAASLTRT   513
Sbjct   361   ISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRN   420

Query   514   NMVLVGTDVPYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV   573
Sbjct   421   HMILVGTDPLYGTMYNHSTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVV   480

Query   574   SMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQ   633
Sbjct   481   TMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKDSLNLQTTAKALEQVSQQ   540

Query   634   SPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKA   693
Sbjct   541   SPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKV   600

Query   694   EEVPDAMYGWTKEATAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLGD   750
Sbjct   601   EEVPDAMYGWTKEATAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLGD   657

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>gb|AA556848.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=671

Score = 1180 bits (3052), Expect = 0.0, Method: Composition-based stats.  
Identities = 607/671 (90%), Positives = 638/671 (95%), Gaps = 0/671 (0%)

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Query   80   YDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVRE   139
Sbjct   1     YDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVRE   60

Query   140   QLSQPNLKQVSFGAKNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIG   199
Sbjct   61   QLSQPNLKQVSFGAKNGGITYANMMAIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIG   120

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Query	200	LAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGK	259
Sbjct	121	LAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGK	180
Query	260	DVYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGIT	319
Sbjct	181	DVYTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTK+GIT	240
Query	320	EDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWDVNEG	379
Sbjct	241	+DFVWRDILYQ NYEPGS MKVM LA++IDNNTFPGGE FNSSE KIAD T RDWDVNEG	300
Query	380	LTGGRRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPA	439
Sbjct	301	LTGG MMTFSQGFHSSNVGM LLE+KMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPA	360
Query	440	DNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIV	499
Sbjct	361	DNIV+IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI+A+YDPNDQT RKSQKEIV	420
Query	500	GNPVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNG	559
Sbjct	421	GNPVSKDAAS TRT MVLVGTDPVYGTMYNHSTGKP VTPVQONVALKSGTAQIADEKNG	480
Query	560	GVLVGLTDYIIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSL	619
Sbjct	481	GVLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLN	540
Query	620	LQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKN	679
Sbjct	541	LQ+ AK L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEGKN	600
Query	680	LAPNQVVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEFQGS GSTVQKQDVRNTAIK	739
Sbjct	601	LAPNQVVL+LSDK EE+PDYMGW KETAE AKWL+IELEF+GSGS VQKQDVR NTAIK	660
Query	740	DIKKITLTLGD 750	
Sbjct	661	+IKKI LTLGD	
		NIKKIKLTLGD 671	

>emb|CAB65446.1| penicillin binding protein 2x [Streptococcus pneumoniae]  
Length=666

Score = 1179 bits (3051), Expect = 0.0, Method: Composition-based stats.  
Identities = 608/666 (91%), Positives = 638/666 (95%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFG+KNGGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	ISSPLQSFMETQMDAF+EKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW	240
Query	325	RDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGG	384
Sbjct	241	RDILYQSNYEPGS MKVMMLAAAIIDNNTFPGGEVFNSSSELKIAD TIRDW+VNEGLTGG	300
Query	385	MMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGV TRFGLTDEYAGQLPADNIVN	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI+A+YDPN+QT R+SQKEIVGNPVS	420
Query	505	KDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	KDAA TRT+MVLVGTDP YGTMYNHSTGK TV VPGONVALKSGTA+IADEKNGGYLVG	480
Query	565	LTDYIIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA	624
Sbjct	481	T+ IFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ A	540
Query	625	KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQ	684
		K L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEG NLAPNQ	

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*   Sbjct   541   KNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQ   600
      Query   685   QVLILSDKAEVDPDYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI   744
      Sbjct   601   QVLLLSDKVEEIPDYGWKKETAETFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNIKKI   660
      Query   745   TLTLGD   750
      Sbjct   661   KLTLDG   666

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>gb|AAN32859.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=661

Score = 1176 bits (3043), Expect = 0.0, Method: Composition-based stats.  
Identities = 606/661 (91%), Positives = 634/661 (95%), Gaps = 0/661 (0%)

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Query   90   DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV   149
Sbjct   1    DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV   60

Query   150   SFGAKGNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG   209
Sbjct   61   SFG+KGNGITYANMM+IKKELE AEVKIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG   120

Query   210   SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPL   269
Sbjct   121  SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVTYTTISSPL   180

Query   270   QSFMETQMDAFQEKVKGKMYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY   329
Sbjct   181  QSFMETQMDAFQEKVKGKMYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY   240

Query   330   QSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWVNEGLTGGRMMTFS   389
Sbjct   241  QSNYEPGS MKVMMLAAAIIDNNTFPGGEVFNSSSELKIADVTIRDWVNEGLTGGRMMTFS   300

Query   390   QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS   449
Sbjct   301  QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS   360

Query   450   FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSCKDAAS   509
Sbjct   361  FGQGISVTQTQMIRAFTAIANDGVMLEPKFITALYDPNNQTVRRSQKEIVGNPVSCKDAAG   420

Query   510   LTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGYLVGLTDYI   569
Sbjct   421  QTRTHMVLVGTDPVYGTMYNHSTGKATVNVPGQONVALKSGTAQIADEKNGGYLVGSTNNI   480

Query   570   FSAVMSSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ   629
Sbjct   481  FSVVAMNPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ AK L++   540

Query   630   VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLIL   689
Sbjct   541  VTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQVLLL   600

Query   690   SDKAEVDPDYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLG   749
Sbjct   601  SDKVEEIPDYGWKKETAETFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTLG   660

Query   750   D   750
Sbjct   661   D   661

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>gb|AA556854.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=666

Score = 1174 bits (3038), Expect = 0.0, Method: Composition-based stats.  
Identities = 607/665 (91%), Positives = 637/665 (95%), Gaps = 0/665 (0%)

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Query   86   PIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPN   145
Sbjct   2    PIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPN   61

Query   146   LKQVSFGAKGNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLAQLHE   205
Sbjct   62   LKQVSFGAKGNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLAQLHE   121

Query   206   NEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTI   265
Sbjct   122  NEDGSKSLLGT G+ESSLN+ILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGKDVTYTT+   181

Query   266   SSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWR   325
Sbjct   266  SSPLQSFMETQMDAF EKVKGKMYMTATLVSAKTGEILATTQRPTF+ADTK+GIT+DFVWR

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Sbjct	182	SSPLQSFMETQMDAFLEKVKGYMTATLVSAKTGEILATTQRPTFNADTKDGITKDFVWR	241
Query	326	DILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRM	385
Sbjct	242	DILYQ NYEPGS MKVM LA++IDNNTFPGGE FNSSE KIAD T RDWDVNEGLTG M	301
Query	386	MTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNI	445
Sbjct	302	MTFSQGFAHSSNVGM LLE+KMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIV+I	361
Query	446	AQSSFQGGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSK	505
Sbjct	362	AQSSFQGGISVTQTQMIRAFTAIANDGVMLEPKFI+A+YDPNDQT RKSQKEIVGNPVSK	421
Query	506	DAASLTRTNMVLVGTDVPYGTMYNHSTGKPTVTVPQGQNVALKSGTAQIADEKNGGYLVGL	565
Sbjct	422	DAASQTRTQMVLVGTDVPYGTMYNHSTGKPIVTVPGQNVALKSGTAQIADEKNGGYLVGP	481
Query	566	TDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAK	625
Sbjct	482	TNYIFSVVAMNPAENPDFILYVTVQQPEH+SGIQLGEFANPILERASAMK+SLNLQ+ AK	541
Query	626	ALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQ	685
Sbjct	542	L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEGKNL+PNQQ	601
Query	686	VLILSDKAEVDPMYGWTKETATLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKIT	745
Sbjct	602	VLILSDKAEVDPMYGWTKETAT AKWLNIELEF+GSGSTVQKQDVRRANTAIKDIKKIT	661
Query	746	LTLGD 750	
Sbjct	662	LTLGD 666	

>gb|AAN32860.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=661

Score = 1174 bits (3038), Expect = 0.0, Method: Composition-based stats.  
Identities = 609/661 (92%), Positives = 635/661 (96%), Gaps = 0/661 (0%)

Query	90	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV	149
Sbjct	1	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKGNGITYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG	209
Sbjct	61	SFG+KNGGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPL	269
Sbjct	121	SKSLLGTSGMESSLNSILAG DGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTTISS L	180
Query	270	QSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	329
Sbjct	181	QSFMETQM+AFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEG+T+DFVWRDILY	240
Query	330	QSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFS	389
Sbjct	241	QSNYEPGSTMKVM LAAAIIDNNTFPGGEVFNSSSELK+ADATIRDWDVNEGLTG MMTFS	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGI PTRFGLTDEYAGQLPADNIVNIAQSS	360
Query	450	FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAAS	509
Sbjct	361	FGQGISVTQTQMIRAFTAIANDGVMLEPKFI+A+YDPN+Q+ RKSQKEIVGNPVSKDAAS	420
Query	510	LTRTNMVLVGTDVPYGTMYNHSTGKPTVTVPQGQNVALKSGTAQIADEKNGGYLVGLTDYI	569
Sbjct	421	TRT+MVLVGTD P YGTMYNHSTGK TV VPGQNVALKSGTA+IADEKNGGYLVG T+ I	480
Query	570	FSVAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
Sbjct	481	FS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERA AMKDSLNLQ+TAK L+Q	540
Query	630	VSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLIL	689
Sbjct	541	V+ QS Y MPS+KDISPGDLAE LRRN+VQPIVVGTGTKIK SS EEG NLAPNQVLL+L	600
Query	690	SDKAEVDPMYGWTKETATLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKITLTLG	749
Sbjct	601	SDKAEVDPMYGWT KATAEAFSKWLNIELVFEGSGSTVQKQDVRRANTAIKDIKKITLTLG	660
Query	750	D 750	



Sbjct 661 D 661

>gb|AA556839.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=670

Score = 1170 bits (3027), Expect = 0.0, Method: Composition-based stats.  
Identities = 603/670 (90%), Positives = 636/670 (94%), Gaps = 0/670 (0%)

Query	81	DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ	140
Sbjct	1	DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ	60
Query	141	LSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGL	200
Sbjct	61	LSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGL	120
Query	201	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKD	260
Sbjct	121	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKD	180
Query	261	VYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITE	320
Sbjct	181	VYTTISSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITE	240
Query	321	DFVWRDILYQSNYEPGSTMKVMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGL	380
Sbjct	241	DFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNDGL	300
Query	381	TGGRMMTFSQGFHSSNVGMLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPAD	440
Sbjct	301	T G MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPAD	360
Query	441	NIVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVG	500
Sbjct	361	NIV+IAQSSFGQGISVTQTOM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVG	420
Query	501	NPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGG	560
Sbjct	421	NPVSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVPQGNVA+KSGTAQIADEKNGG	480
Query	561	YLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL	620
Sbjct	481	YLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNL	540
Query	621	QTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAAEEGKNL	680
Sbjct	541	Q+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEG NL	600
Query	681	APNQOVLILSDKAAEVPDYGWTKETAETLAKWLNIELEFGSGSTVQKQDVNRANTAIKD	740
Sbjct	601	APNQOVL+LSDK EE+PDYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+	660
Query	741	IKKITLTLGD 750	
Sbjct	661	IKKITLTLGD 670	

>emb|CAB65445.1| penicillin binding protein 2x [Streptococcus pneumoniae]  
Length=666

Score = 1170 bits (3026), Expect = 0.0, Method: Composition-based stats.  
Identities = 599/665 (90%), Positives = 636/665 (95%), Gaps = 0/665 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVE+TQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFG+KNGITYANMM++KKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTK+GIT+DFVW	240
Query	325	RDILYQSNYEPGSTMKVMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGR	384
Sbjct	241	RDILYQSNYEPGSAMKVMTLAASIDNNTFPGGEYFNSSSELKIADATIRDWDVNDGLTTGG	300
Query	385	MMTFSQGFHSSNVGMLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444

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Sbjct 301 MMTFSQGFAHSSNVGM+LLEQKMGD TWLDYLNRFKFGVPTRFGLTDEY+GQLPADNIVN 360
MMTFSQGFAHSSNVGMSLLEQKMGD TTWLDYLNRFKFGVPTRFGLTDEYSGQLPADNIVN

Query 445 IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS 504
IA S+FGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVG PVS
Sbjct 361 IAMSAFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGKPV 420
IAMS+FGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYD TNNQSVRKSQKEIVGKPV

Query 505 KDAASLRTNMTMLVLTGDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVG 564
+DAASLRTNMTMLVLTGDP+YGTMYNH TGKP +TVPGQNVALKSGTA+IADEKNGGYLVG
Sbjct 421 EDAASLRTNMTMLVLTGDPYGTMYNHSTGKPIITVPQNVALKSGTAQIADEKNGGYLVG 480
EDAASLRTNMTMLVLTGDPYGTMYNHSTGKPIITVPQNVALKSGTAQIADEKNGGYLVG

Query 565 LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA 624
T+YIF V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ A
Sbjct 481 STNYIFPVVMTMNPENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPA 540
STNYIFPVVMTMNPENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPA

Query 625 KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTTIKNSSAEEGKNLAPNQ 684
K L+QV+ +S Y MPS+KDISPGDLAE LRRN+VQPIVVGTGTTIK SS EEG NLAPNQ
Sbjct 541 KNLDQVTTTESSYAMPSIKDISPGDLAEALRRNIVQPIVVGTGTTIKESSVEEGTNLAPNQ 600
KNLDQVTTTESSYAMPSIKDISPGDLAEALRRNIVQPIVVGTGTTIKESSVEEGTNLAPNQ

Query 685 QVLILSDKAAEVPDMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKI 744
QV++LSDK EE+PDMYGTWKETAET AKWLNIELEF+GSGSGSTVQKQDVRRANTAIKDIKKI
Sbjct 601 QVLLSDKVEEIPDMYGTWKETAETFAKWLNIIELEFEGSGSGSTVQKQDVRRANTAIKDIKKI 660
QVLLSDKVEEIPDMYGTWKETAETFAKWLNIIELEFEGSGSGSTVQKQDVRRANTAIKDIKKI

Query 745 TLTLG 749
TLTLG
Sbjct 661 TLTLG 665
TLTLG

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>emb|CAA67013.1| penicillin-binding protein [Streptococcus pneumoniae]  
Length=666

Score = 1169 bits (3024), Expect = 0.0, Method: Composition-based stats.  
Identities = 602/666 (90%), Positives = 633/666 (95%), Gaps = 0/666 (0%)

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Query 85 VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 144
VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYL MEESYVREQLSQP
Sbjct 1 VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLAMEESYVREQLSQP 60
VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLAMEESYVREQLSQP

Query 145 NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH 204
NLKQVSFGAKGNGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH
Sbjct 61 NLKQVSFGAKGNGITYANMMAIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH 120
NLKQVSFGAKGNGITYANMMAIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH

Query 205 ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR LGNIVPGTEQVSQRTMDGKDVYTT 264
ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR+GNIIVPGTE VSQ+T+DGKDVYTT
Sbjct 121 ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRVGNIVPGTELVVSQQTVDGKDVYTT 180
ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRVGNIVPGTELVVSQQTVDGKDVYTT

Query 265 ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITDFVW 324
+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTK+GIT+DFVW
Sbjct 181 LSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKDGITKDFVW 240
LSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKDGITKDFVW

Query 325 RDILYQSNYEPGSTMKVMMMLAAAIDNNTFPGGEVFNSSSELKIADATIRDWVNEGLTGG 384
RDILYQ NYEPGS MKVMMMLA++IDNNTFPGGE FNSSE KIAD T RDWVNEGLTGG
Sbjct 241 RDILYQGNYEPGSAMKVMMMLASSIDNNTFPGGEYFNSSSESKIADVTTTRDWVNEGLTGG 300
RDILYQGNYEPGSAMKVMMMLASSIDNNTFPGGEYFNSSSESKIADVTTTRDWVNEGLTGG

Query 385 MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN 444
MMTFSQGFAHSSNVGM LLE+KMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIV+
Sbjct 301 MMTFSQGFAHSSNVGMILLEEKMGD TTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVS 360
MMTFSQGFAHSSNVGMILLEEKMGD TTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVS

Query 445 IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS 504
IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI+A+YDPNDQT RKSQKEIVGNPVS
Sbjct 361 IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFITALYDPNDQTVRKSQKEIVGNPVS 420
IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFITALYDPNDQTVRKSQKEIVGNPVS

Query 505 KDAASLRTNMTMLVLTGDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVG 564
KDAAS TRT MVLVLTGDPVYGTMYNHSTGKP VTVPQNVALKSGTAQIADEKNGGYLVG
Sbjct 421 KDAASQTRTQMVLVLTGDPVYGTMYNHSTGKPIITVPQNVALKSGTAQIADEKNGGYLVG 480
KDAASQTRTQMVLVLTGDPVYGTMYNHSTGKPIITVPQNVALKSGTAQIADEKNGGYLVG

Query 565 LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA 624
T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ A
Sbjct 481 PTNYIFSVMNPENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPA 540
PTNYIFSVMNPENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPA

Query 625 KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTTIKNSSAEEGKNLAPNQ 684
K L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTTIK +S EEGKNLAPNQ
Sbjct 541 KNLDQVTTTESSYAMPSIKDISPGELAE LRRNIVQPIVVGTGTTIKETSVEEGKNLAPNQ 600
KNLDQVTTTESSYAMPSIKDISPGELAE LRRNIVQPIVVGTGTTIKETSVEEGKNLAPNQ

Query 685 QVLILSDKAAEVPDMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKI 744
QVL+LSDK EE+PDMYGTWKETAET AKWL+IELEF+GSGS VQKQDVRR NTAIK+IKKI
Sbjct 601 QVLLSDKVEEIPDMYGTWKETAETFAKWL DIELEFEGSGSIVQKQDVRRNTAIKNIKKI 660
QVLLSDKVEEIPDMYGTWKETAETFAKWL DIELEFEGSGSIVQKQDVRRNTAIKNIKKI

Query 745 TLTLGD 750
LTLGD
Sbjct 661 KLTLGD 666
KLTLGD

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>gb|AA556838.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=670

Score = 1165 bits (3014), Expect = 0.0, Method: Composition-based stats.  
Identities = 601/670 (89%), Positives = 635/670 (94%), Gaps = 0/670 (0%)

Query	81	DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ	140
Sbjct	1	DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ	60
Query	141	LSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGL	200
Sbjct	61	LSQPNLKQVSFGAKGNGITYANMMSIKKELEAEVKGIDFTTSPNRSYPNGQFASSFIGL	120
Query	201	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD	260
Sbjct	121	AQLHENEDGSKSLLGTSGMESSLNSILAGDGIITYEKDRLGNIVPGTEQVSQ+T+DGKD	180
Query	261	VYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPFTDADTKEGITE	320
Sbjct	181	VYTTISSLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPFTFNADTKEGITE	240
Query	321	DFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFNSELKIADATIRDWDVNEGL	380
Sbjct	241	DFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPGGEVFNSEFKIADATIRDWDVNDGL	300
Query	381	TGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTREFGLTDEYAGQLPAD	440
Sbjct	301	TGGRMMTFLQGFHSSNVGMSLLEQKMGDATWLDYLNRFKFGVPTREFGLTDEYAGQLPAD	360
Query	441	NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVG	500
Sbjct	361	NIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVG	420
Query	501	NPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGG	560
Sbjct	421	NPVSKAAASTTRNHMILVGTDPVYGTMYNHSTGKPIITVPGQNVAVKSGTAQIADEKNGG	480
Query	561	YLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL	620
Sbjct	481	YLVGSTNYIFSVVVTMNPENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNL	540
Query	621	QTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGKTIKNSSAEEGKNL	680
Sbjct	541	QSPAKNLQVTTTESSYAMPSIKDISPGDLAEELRRNLVQPIVVGTGKTIKETSVEEGTNL	600
Query	681	APNQVVLILSDKAEVPMYGTWKETAETLAKWLNIELEFGSGSTVQKQDVRANTAIKD	740
Sbjct	601	APNQVVLILSDKVEEIPMYGWWKETAETFAKWLIDIELEFGSGSVVQKQDVRANTAIKD	660
Query	741	IKKITLTLGD 750	
Sbjct	661	IKKITLTLGD 670	

>emb|CAB65442.1| penicillin binding protein 2x [Streptococcus pneumoniae]  
Length=666

Score = 1165 bits (3014), Expect = 0.0, Method: Composition-based stats.  
Identities = 597/666 (89%), Positives = 630/666 (94%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITYANMMSIKKELEAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPFTDADTKEGITEFVW	324
Sbjct	181	ISSTLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPFTDADTKEGITEFVW	240
Query	325	RDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFNSELKIADATIRDWDVNEGLTGGR	384
Sbjct	241	RDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFNSELKIADATIRDWDVNEGLTGGR	300
Query	385	MMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTREFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFLQGFALSSNVGMSLLEQKMGDATWLDYLNRFKFGVPTREFGLTDEYAGQLPADNIVN	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFITALYDPNDQTVRRSQKEIVGNPVS	420

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Query 505 KDAASLRTNMTVLVGTDPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG 564
          KDAASLRT+MVLVGTDP YGTMYNH TGKP +TVPGQNVA+KSGTA+IADEKNGGYLVG
Sbjct 421 KDAASLRTHTMVLVGTDPYGTMYNHGTGKPIITVPGQNVAVKSGTAEIADEKNGGYLVG 480

Query 565 LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA 624
          T+YIFS VSM+PAENPDFILYVT+QQPEHYS + LGEFANPILERASAMK+SLNLQ+ A
Sbjct 481 ATNYIFSVMNPAENPDFILYVTIQQPEHYSVVHLGEFANPILERASAMKESLNLQSPA 540

Query 625 KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQ 684
          K LEQV+ +S Y MPS+KDISPGDLAE LRRN+VQPIV+GTGTGIK SS EEGKNL PNQ
Sbjct 541 KNLEQVTAESSYAMPSIKDISPGDLAEALRRNIVQPIVIGTGTGIKESSVEEGKNLVPNQ 600

Query 685 QVLILSDKAAEEVPDYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKI 744
          QVL+LSDK EE+PDYGW KETAE AKWL+IELEF+GSGS VQ+QDVRRANT IK+IK I
Sbjct 601 QVLLLSDKVEEIPDYGWKKETAEAFKWLIDIELEFEGSGSIVQKQDVRRANTTIKNIKNI 660

Query 745 TLTLGD 750
          LTLGD
Sbjct 661 KLTLGD 666

```

>emb|CAB65443.1| penicillin binding protein 2x [Streptococcus pneumoniae]  
Length=666

Score = 1162 bits (3007), Expect = 0.0, Method: Composition-based stats.  
Identities = 601/666 (90%), Positives = 634/666 (95%), Gaps = 0/666 (0%)

```

Query 85 VPAAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 144
          VPAAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP
Sbjct 1 VPAAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 60

Query 145 NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH 204
          NLKQVSFGAKGNGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH
Sbjct 61 NLKQVSFGAKGNGITYANMMSIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH 120

Query 205 ENEDGSKSLGTSMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT 264
          ENEDGSKSLGTSMESSLNSILAG DGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT
Sbjct 121 ENEDGSKSLGTSMESSLNSILAGKDGIIITYEKDRLGNIVPGTEQVSQQTVDGKDVYTT 180

Query 265 ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW 324
          ISS LQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEG+T+DFVW
Sbjct 181 ISSTLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGLTKDFVW 240

Query 325 RDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGR 384
          RDILYQSNYEPGSTMKVM LA++ID+NTFP GE FNSSELKIADATIRDWDVN+GLT G
Sbjct 241 RDILYQSNYEPGSTMKVMTLASSIDSNTFPGGEVFNSSSELKIADATIRDWDVNDGLTTGG 300

Query 385 MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN 444
          MMTF QGFA+SSNVGM+LLEQKMGDATWLDYLNRFKFGVPTRFGLTDEY+GQLPADNIVN
Sbjct 301 MMTFLQGFAYSNVGMSLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYSGQLPADNIVN 360

Query 445 IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS 504
          IA S+FGQGISVTQTQM+RAFTAIANDGVMLEPKFISA+YDPNDQT RKSQKEIVGNPVS
Sbjct 361 IAMSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISALYDPNDQTVRKSQKEIVGNPVS 420

Query 505 KDAASLRTNMTVLVGTDPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG 564
          KDAAS TRT+MVLVGTDP YGTMYNHSTGK TV VPGQNVALKSGTA+IADEKNGGYLVG
Sbjct 421 KDAASQTRTHMVLVGTDPYGTMYNHSTGKATVNVPGQNVALKSGTAEIADEKNGGYLVG 480

Query 565 LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA 624
          T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ A
Sbjct 481 STNYIFSVMNPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPA 540

Query 625 KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQ 684
          K L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTGIK +S EEGKNLAPNQ
Sbjct 541 KNLDQVTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTGIKETSVEEGKNLAPNQ 600

Query 685 QVLILSDKAAEEVPDYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKI 744
          QVL+LSDK EE+PDYGW KETAE AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI
Sbjct 601 QVLLLSDKVEEIPDYGWKKETAEAFKWLIDIELEFEGSGSIVQKQDVRRNTAIKNIKKI 660

Query 745 TLTLGD 750
          LTLGD
Sbjct 661 KLTLGD 666

```

>gb|AA56842.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=669

Score = 1160 bits (3000), Expect = 0.0, Method: Composition-based stats.  
Identities = 597/669 (89%), Positives = 633/669 (94%), Gaps = 0/669 (0%)

```

Query 82 RNVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL 141
          RNVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL
Sbjct 1 RNVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL 60

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Query 142 SQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA 201
Sbjct 61 SQPNLKQVSFGAKGNIGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLA 120
SQPNLKQVSFGAKGNIGITYANMMAIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGLA

Query 202 QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV 261
Sbjct 121 QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDV 180
QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDV

Query 262 YTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPFTDADTKEGITED 321
Sbjct 181 YTTISSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPFT+ADTKEGITED 240
YTTISSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPFTNADTKEGITED

Query 322 FVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLT 381
Sbjct 241 FVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT 300
FVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNDGLT

Query 382 GGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN 441
Sbjct 301 G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADN 360
TGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRKFGVPTRFGLTDEYAGQLPADN

Query 442 IVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQQEIVGN 501
Sbjct 361 IV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQQEIVGN 420
IVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQQEIVGN

Query 502 PVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGGY 561
Sbjct 421 PVSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVPGQNV+A+KSGTAQIADEKNGGY 480
PVSKEAASTTRNHMILVGTDPVYGTMYNHYTGKPIITVPQGNVAVKSGTAQIADEKNGGY

Query 562 LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ 621
Sbjct 481 LVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ 540
LVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQ

Query 622 TTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA 681
Sbjct 541 + AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEG NLA 600
SPAKNLDKVTTESYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLA

Query 682 PNQQVLILSDKAEVDPMYGWTKETATLAKWLNIELEFQSGSGSTVQKQDVRANTAIDKI 741
Sbjct 601 PNQQVL+LSDK EE+PDYMGW KETAT AKWL+IELEF+GSGS VQKQDVR NTAIK+I 660
PNQQVLLLSDKVEEIPDYGWKKETATFAKWLIDIELEFEGSGSVVQKQDVRTNTAIKNI

Query 742 KKITLTLGD 750
Sbjct 661 KKI LTLGD 669
KKIKLTLGD

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>gb|AA556852.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=670

Score = 1158 bits (2996), Expect = 0.0, Method: Composition-based stats.  
Identities = 596/670 (88%), Positives = 632/670 (94%), Gaps = 0/670 (0%)

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Query 81 DRNGVPPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ 140
Sbjct 1 DRNGVPPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ 60
DRNGVPPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ

Query 141 LSQPNLKQVSFGAKGNIGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGL 200
Sbjct 61 LSQPNLKQVSFGAKGNIGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGL 120
LSQPNLKQVSFGAKGNIGITYANMMTIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGL

Query 201 AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD 260
Sbjct 121 AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTE VSQ+T+DGKD 180
AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTELVSQQTVDGKD

Query 261 VYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPFTDADTKEGITE 320
Sbjct 181 VYTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPFT+ADTKEGITE 240
VYTTLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPFTNADTKEGITE

Query 321 DFVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGL 380
Sbjct 241 DFVWRDILYQSNYEPGS KVMMLA++IDNNTFP GE FNSSE KIADAT RDWDVNEGL 300
DFVWRDILYQSNYEPGSFAKVMMLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNEGL

Query 381 TGGMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPAD 440
Sbjct 301 T G MMTFSGQFAHSSNVG +LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPAD 360
TTGGMMTFSQGFAHSSNVGTSLLLEQKMGDATWLDYLKRKFGVPTRFGLTDEYAGQLPAD

Query 441 NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQQEIVG 500
Sbjct 361 NIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQQEIVG 420
NIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQQEIVG

Query 501 NPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGG 560
Sbjct 421 NPVSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVPGQNV+A+KSG AQIADEKNGG 480
NPVSKEAASTTRNHMILVGTDPVYGTMYNHYTGKPIITVPQGNVAVKSGAAQIADEKNGG

Query 561 YLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL 620
Sbjct 481 YLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNL 540
YLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNL

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Query   621  QTTAKALEQVSQQSPYPMPVSKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNL 680
      Q+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEG NL
Sbjct   541  QSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNL 600

Query   681  APNQQVLILSDKAAEVPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDV RANTAIKD 740
      APNQQVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDV R NTAIK+
Sbjct   601  APNQQVLLLSDKVVEEIPDMYGWKKETAETFAKWLDIELEFEGSGSVVQKQDV RNTAIKN 660

Query   741  IKKITLTLGD 750
      IKKI LTLGD
Sbjct   661  IKKIKLTLGD 670

```

>emb|CAB65441.1| penicillin binding protein 2x [Streptococcus pneumoniae]  
Length=666

Score = 1157 bits (2992), Expect = 0.0, Method: Composition-based stats.  
Identities = 597/666 (89%), Positives = 631/666 (94%), Gaps = 0/666 (0%)

```

Query   85  VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 144
      VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP
Sbjct   1  VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 60

Query   145  NLKQVSFGAKGNGITYANMMSIKKELEAAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH 204
      NLKQVSFGAKGNGITYANMMSIKKELE AEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH
Sbjct   61  NLKQVSFGAKGNGITYANMMSIKKELETAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH 120

Query   205  ENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT 264
      ENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT
Sbjct   121  ENEDGSKSLLGTSGMESSLNSILAGKDGIIITYEKDRLGNIVPGTEQVSQQTVDGKDVYTT 180

Query   265  ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW 324
      ISS LQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVW
Sbjct   181  ISSTLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFVW 240

Query   325  RDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGR 384
      RDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G
Sbjct   241  RDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFNSSSEFKIADATTRDWDVNDGLTTGG 300

Query   385  MMTFSQGFAHSSNVGMTLLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN 444
      MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+
Sbjct   301  MMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVS 360

Query   445  IAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS 504
      IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS
Sbjct   361  IAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVS 420

Query   505  KDAASLRTNMVLVGTDVPYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGGYLVG 564
      K+AAS TR +M+LVGTDV+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG
Sbjct   421  KEAASLRTNMILVGTDPLYGTMYNHYTGKPIITVPQGNVAVKSGTAQIADEKNGGYLVG 480

Query   565  LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA 624
      T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ A
Sbjct   481  STNYIFSVMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPA 540

Query   625  KALEQVSQQSPYPMPVSKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQ 684
      K L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEG NLAPNQ
Sbjct   541  KNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQ 600

Query   685  QVLILSDKAAEVPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDV RANTAIKDIKKI 744
      QVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDV RANTAIKDIKKI
Sbjct   601  QVLLLSDKVVEEIPDMYGWKKETAETFAKWLDIELEFEGSGSVVQKQDV RANTAIKDIKKI 660

Query   745  TLTLGD 750
      TLTLGD
Sbjct   661  TLTLGD 666

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>gb|AAN32855.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=661

Score = 1157 bits (2992), Expect = 0.0, Method: Composition-based stats.  
Identities = 598/661 (90%), Positives = 630/661 (95%), Gaps = 0/661 (0%)

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Query   90  DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLQKV 149
      DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLQKV
Sbjct   1  DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLQKV 60

Query   150  SFGAKGNGITYANMMSIKKELEAAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG 209
      SFGAKGNGITYANMMSIKKELE AEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG
Sbjct   61  SFGAKGNGITYANMMSIKKELETAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG 120

Query   210  SKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPL 269
      SKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTTISS L
Sbjct   121  SKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQQTVDGKDVYTTISSTL 180

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Query	270	QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	329
Sbjct	181	QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEG+T+DFVWRDILY	240
Query	330	QSNYEPGSTMKVMMLAAAIIDNNTFPGGGEVFNSELKIADATIRDWDVNEGLTGGRMMTFS	389
Sbjct	241	QSNYEPGSTMKVM LA++IDNNTFP GE FNSSELKIADATIRDWDVN+GLT G MMTF	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGMLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEY+GQLPADNIVNIA S+	360
Query	450	FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSCKDAAS	509
Sbjct	361	FGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYDPNDQT RKSQKEIVGNPVSCKDAAS	420
Query	510	LTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYI	569
Sbjct	421	QTRTHMVLVGTDPRYGTMYNHSTGKATVNVPGQNVALKSGTAQIADEKNGGYLVGSTNYI	480
Query	570	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
Sbjct	481	FS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ AK L+Q	540
Query	630	VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLIL	689
Sbjct	541	V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEGKNLAPNQVLL+L	600
Query	690	SDKAEVVPDMPYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRNTAIKDIKKITLTG	749
Sbjct	601	SDK EE+PDMPYGW KETAE AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTG	660
Query	750	D 750	
Sbjct	661	D 661	

>gb|AA556849.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=669

Score = 1155 bits (2987), Expect = 0.0, Method: Composition-based stats.  
Identities = 594/669 (88%), Positives = 632/669 (94%), Gaps = 0/669 (0%)

Query	82	RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL	141
Sbjct	1	RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL	60
Query	142	SQPNLKQVSFSGAKNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA	201
Sbjct	61	SQPNLKQVSFG+KNGGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLA	120
Query	202	QLHENEDGSKSLLGTSGMESSLSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV	261
Sbjct	121	QLHENEDGSKSLLGTSGMESSLSILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGKDV	180
Query	262	YTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITED	321
Sbjct	181	YTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITED	240
Query	322	FVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGGEVFNSELKIADATIRDWDVNEGLT	381
Sbjct	241	FVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT	300
Query	382	GGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN	441
Sbjct	301	G MMTF QGFAHSSNVGMLLEQKMGDATWLDYL RKFVGVPTRFGLTDEYAGQLPADN	360
Query	442	IVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN	501
Sbjct	361	IV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGN	420
Query	502	PVSCKDAASLRTTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGY	561
Sbjct	421	PVSK+AAS TR +M+LVGTDVP+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGY	480
Query	562	LVGLTDYIIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ	621
Sbjct	481	LVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ	540
Query	622	TTAKALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA	681
Sbjct	541	+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEG NLA	600
Query	682	PNQQVLLILSDKAEVVPDMPYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRNTAIKDI	741
		PNQQVL+LSDK EE+PDMPYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+I	



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* Sbjct 601 PNQQVLLLSDKVEEIPDMYGWKKETAETFAKWLKDIELEFEGSGSVVQKQDVRTNTAIKNI 660
Query 742 KKITLTLGD 750
      KKI LTLGD
- Sbjct 661 KKIKLTLGD 669

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>gb|AA556851.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=668

Score = 1152 bits (2980), Expect = 0.0, Method: Composition-based stats.  
Identities = 593/668 (88%), Positives = 631/668 (94%), Gaps = 0/668 (0%)

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Query 83  NGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLS 142
Sbjct 1   NGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLS 60

Query 143 QPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQ 202
Sbjct 61  QPNLKQVSFG+KNGGITYANMMSIKKELE AEVKIGIDFTTSPNRSYPNGQFASSFIGLAQ 120
      QPNLKQVSFGSKGNGITYANMMSIKKELETAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQ

Query 203 LHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDR LGNIVPGTEQVSQRTMDGKDVY 262
Sbjct 121 LHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDR+GNIVPGTE VSQ+T+DGKDVY 180
      LHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRVGNIVPGTELVSQQTVDGKDVY

Query 263 TTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDF 322
Sbjct 181 TT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDF 240
      TTLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITEDF

Query 323 VWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTG 382
Sbjct 241 VWRDILYQSNYEPGSAMKVMTLASSIDNNTFPGSEYFNSSEFKIADATTRDWDVNDGLTT 300
      VWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTG

Query 383 GRMMTF SQGFAHSSNVGMTLLLEQKMGD ATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNI 442
Sbjct 301 G MMTF QGFAHSSNVGM+LLEQKMGD ATWLDYL RKFVGVPTRFGLTDEYAGQLPADNI 360
      GGMMTF LQGFAHSSNVGMSLLEQKMGD ATWLDYLRKFVGVPTRFGLTDEYAGQLPADNI

Query 443 VNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNP 502
Sbjct 361 V+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNP 420
      VSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNP

Query 503 VSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGGYL 562
Sbjct 421 VSK+AAS TR +M+LVGTD P+YGTMYNH TGKP +TVPGQNV A+KSGTAQIADEKNGGYL 480
      VSKEAASLRTNMILVGTDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGGYL

Query 563 VGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQT 622
Sbjct 481 VG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ 540
      VGSTNYIFSVVTMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQS

Query 623 TAKALEQVSQQSPYPMPVSKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAP 682
Sbjct 541 AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTGIK +S EEG NLAP 600
      PAKNLDKVTTESSYAMPSIKDISPGELAEALRRNLVQPIVVGTGTGIKETSVEEGTNLAP

Query 683 NQQVLILSDKAAEVPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRNTAIKDIK 742
Sbjct 601 NQQVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IK 660
      NQQVLLLSDKVEEIPDMYGWKKETAETFAKWLKDIELEFEGSGSVVQKQDVRTNTAIKNIK

Query 743 KITLTLGD 750
Sbjct 661 KIKLTLGD 668

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>gb|AA556841.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=674

Score = 1150 bits (2974), Expect = 0.0, Method: Composition-based stats.  
Identities = 592/674 (87%), Positives = 634/674 (94%), Gaps = 0/674 (0%)

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Query 77  GTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESY 136
Sbjct 1   GTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFNKVAEVFHKYLDME+E+Y 60
      GTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFNKVAEVFHKYLDMEDEAY

Query 137 VREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKIGIDFTTSPNRSYPNGQFASS 196
Sbjct 61  V+EQLSQPNL QVSFGAKGNGITYANMM+IKK+L+ A ++GIDFTTSPNRSYPNGQFASS 120
      VKEQLSQPNLTQVSFGAKGNGITYANMMAIKKDLKDASIEGIDFTTSPNRSYPNGQFASS

Query 197 FIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDR LGNIVPGTEQVSQRTM 256
Sbjct 121 FIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR LGNIVPGTEQVSQ+T+ 180
      FIGLAQLHENEDGSKSLLGTSGMESSLNSILAGDKDGIITYEKDR LGNIVPGTEQVSQQTV

Query 257 DGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKE 316
Sbjct 181 DGKDVYTTISS LQSFMETQM+AF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKE 240
      DGKDVYTTISS TLQSFMETQMNAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKE

Query 317 GITEDFVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDV 376
      GITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDV

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Sbjct	241	GITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFNSSEFKIADATTRDWDV	300
Query	377	NEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQ N+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQ	436
Sbjct	301	NDGLTTGGMFTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRKFKFGVPTRFGLTDEYAGQ	360
Query	437	LPADNIVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSOK LPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQK	496
Sbjct	361	LPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQK	420
Query	497	EIVGNPVSCKDAASLTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADE EIVGNPVSCK+AAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNV+A+KSGTAQIADE	556
Sbjct	421	EIVGNPVSKEAASSTRNHMILVGTDPLYGTMYNHSTGKPIITVPGQNVAVKSGTAQIADE	480
Query	557	KNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKD KNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+	616
Sbjct	481	KNGGYLVGSTNYIFSVMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKE	540
Query	617	SLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGKTIKNSSAEE SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGKTIK +S EE	676
Sbjct	541	SLNLQSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNLVQPIVVGTGKTIKETSVEE	600
Query	677	GKNLAPNQVVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANT G NLAPNQVVLILSDKAEVPMYGTWKETAETLAKWLNIELEF+GSGS VQKQDVR NT	736
Sbjct	601	GTNLAPNQVVLILSDKAEVPMYGTWKETAETLAKWLNIELEFEGSGSVVQKQDVRTNT	660
Query	737	AIKDIKKITLTLGD 750 AIK+IKKI LTLGD	
Sbjct	661	AIKNIKKIKLTLGD 674	

>emb|CAA88920.1| penicillin-binding protein 2x [Streptococcus pneumoniae]  
Length=666

Score = 1149 bits (2973), Expect = 0.0, Method: Composition-based stats.  
Identities = 592/666 (88%), Positives = 628/666 (94%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGDFTTSPNRSYPNGQFASSFIGLAQLH NLKQVSFGAKGNGITYANMM+IKKELE AEVKGDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITYANMMTIKKELETAEVKGDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIIVPGTEQVSQRTMDGKDVYTT ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIIVPGTE VSQ+T+DGKDVYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIIVPGTELVSQQTVDGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW +SSPLQSFMETQMDAF EKVKGKGYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVW	324
Sbjct	181	LSSPLQSFMETQMDAFLEKVKGKGYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFVW	240
Query	325	RDILYQSNYEPGSTMKVMMLAAAIDNNTFPFGGEVFNSELKIADATIRDWDVNEGLTGGR RDILYQSNYEPGS KVMMLA++IDNNTFP GE FNSSE KIADAT RDWDVNEGLT G	384
Sbjct	241	RDILYQSNYEPGSFAKVMMLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNEGLTTGG	300
Query	385	MMTFSQGFAGHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN MMTFSQGFAGHSSNVG +LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+	444
Sbjct	301	MMTFSQGFAGHSSNVGTSLLLEQKMGDATWLDYLRKFKFGVPTRFGLTDEYAGQLPADNIVS	360
Query	445	IAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSOKKEIVGNPVS IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVS	420
Query	505	KDAASLTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG K+AAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNV+A+KSG AQIADEKNGGYLVG	564
Sbjct	421	KEAASSTRNHMILVGTDPLYGTMYNHSTGKPIITVPGQNVAVKSGAAQIADEKNGGYLVG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ A	624
Sbjct	481	STNYIFSVMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPA	540
Query	625	KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGKTIKNSSAEEGKNLAPNQ K L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGKTIK +S EEG NLAPNQ	684
Sbjct	541	KNLDKVTTESSYAMPSIKDISPGELAEALRRNLVQPIVVGTGKTIKETSVEEGTNLAPNQ	600
Query	685	QVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIAKDIKKI QVL+LSDK EE+PDYMGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI	744
Sbjct	601	QVLLLSDKVEEIPDMYGWKKETAETFAKWLDIELEFEGSGSVVQKQDVRTNTAIAKNIKKI	660
Query	745	TLTLGD 750 LTLGD	
Sbjct	661	KLTLGD 666	

>emb|CAA88919.1| penicillin-binding protein 2x [Streptococcus pneumoniae]  
Length=666

Score = 1149 bits (2971), Expect = 0.0, Method: Composition-based stats.  
Identities = 592/666 (88%), Positives = 628/666 (94%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITYANMM+IKKELE AEVKIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTE VSQ+T+DGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	LSSPLQSFMETQMDAFLEKVKGYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFVW	240
Query	325	RDILYQSNYEPGSTMKVMMMLAAAIIDNNTFPGGGEVFNSSSELKIADATIRDWDVNEGLTGGR	384
Sbjct	241	RDILYQSNYEPGS KVMMLA++IDNNTFP GE FNSSE KIADAT RDWDVNEGLT G	300
Query	385	MMTFSQGFHSSNVGMTLLLEQKMGDATWLDYLNRFKFGVPTFRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFSQGFHSSNVGTSLLLEQKMGDATWLDYLNRFKFGVPTFRFGLTDEYAGQLPADNIVS	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS	420
Query	505	KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	KEAASLRTNMILVGTDPVYGTMYNHSTGKPIITVPQNVA+KSGTAQIADEKNGGYLVG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA	624
Sbjct	481	T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ A	540
Query	625	KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTTGKIKNSSAEEGKNLAPNQ	684
Sbjct	541	K L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTTGKIK +S EEG NLAPNQ	600
Query	685	QVLILSDKAAEEVPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI	744
Sbjct	601	QVLLLSDKVEEIPDMYSWKKETAEETFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNIKKI	660
Query	745	TLTLGD 750	
Sbjct	661	LTLGD 666	

>emb|CAB65448.1| penicillin binding protein 2x [Streptococcus pneumoniae]  
Length=666

Score = 1148 bits (2970), Expect = 0.0, Method: Composition-based stats.  
Identities = 594/666 (89%), Positives = 627/666 (94%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITYANMMSIKKELE AEVKIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	ISS LQSFMETQMDAF EKVKGKGYMTATLVSAKTGEILATTQRPTF+ADTKEGIT+DFVW	240
Query	325	RDILYQSNYEPGSTMKVMMMLAAAIIDNNTFPGGGEVFNSSSELKIADATIRDWDVNEGLTGGR	384
Sbjct	241	RDILYQSNYEPGS MKVM LAAAIIDNNTFP GE FNSSE KIADAT RDWDVN GLT G	300
Query	385	MMTFSQGFHSSNVGMTLLLEQKMGDATWLDYLNRFKFGVPTFRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFLQGFHSSNVGMSLLLEQKMGDATWLDYLNRFKFGVPTFRFGLTDEYAGQLPADNIVS	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504

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Sbjct 361 IAQSSFGQGISVTQTQM+RA TAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS 420
IAQSSFGQGISVTQTQMLRALTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVS

Query 505 KDAASLRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG 564
K+AAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNVA+KSGTAQIADEKNGGYLVG
Sbjct 421 KEAASLRTNMILVGTDPLYGTMYNHSTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVG 480

Query 565 LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA 624
T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ A
Sbjct 481 STNYIFSVMTPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPA 540

Query 625 KALEQVSQQSPYPMPVSKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQ 684
K L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTGIK +S EEG NLAPNQ
Sbjct 541 KNLDKVTTESSYAMPSIKDISPGDLAEELRRNLVQPIVVGTGTGIKETSVEEGTNLAPNQ 600

Query 685 QVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI 744
QVL+LSDK EE+PMYGTWKETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI
Sbjct 601 QVLLSDKVEEIPMYGWWKETAETFAKWLIDIELEFEGSGSVVQKQDVRTNTAIKNIKKI 660

Query 745 TLTLGD 750
LTLGD
Sbjct 661 KLTLGD 666

```

>emb|CAA67012.1| penicillin-binding protein [Streptococcus pneumoniae]  
Length=666

Score = 1148 bits (2970), Expect = 0.0, Method: Composition-based stats.  
Identities = 590/666 (88%), Positives = 631/666 (94%), Gaps = 0/666 (0%)

```

Query 85 VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 144
VPIAEDATSYNVYAVID+ YKSATGKILYVE +QFNKVAEVFHKYLDME+E+YV+EQL+QP
Sbjct 1 VPIAEDATSYNVYAVIDKKYKSATGKILYVEDSQFNKVAEVFHKYLDMEAYVKEQLAQP 60

Query 145 NLKQVSFGAKNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH 204
NL QVSFGAK NGITYANMM+IKK+L+ A V+GIDFTTSPNRSYPNGQFASSFIGLAQLH
Sbjct 61 NLQVSFGAKENGITYANMMMAIKKDLKSDASVEGIDFTTSPNRSYPNGQFASSFIGLAQLH 120

Query 205 ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR LGNIVPGTEQVSQRTMDGKDVYTT 264
ENEDGSKSLLGT G+ESSLN+ILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGKDVYTT
Sbjct 121 ENEDGSKSLLGTGLESSLNTILAGTDGIITYEKDRVGNIVPGTELVSQQTVDGKDVYTT 180

Query 265 ISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITDFVW 324
+SSPLQSFMETQMDAF EKVKGYMTATLVSAKTGEILATTQRPTF+ADTK+GIT+DFVW
Sbjct 181 LSSPLQSFMETQMDAFLEKVKGYMTATLVSAKTGEILATTQRPTFNADTKDGITKDFVW 240

Query 325 RDILYQSNYEPGSTMKVMMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGR 384
RDILYQ NYEPGS MKVM LA++IDNNTFPGGE FNSSE KIAD T RDWDVNEGLTGGR
Sbjct 241 RDILYQGNYEPGSAMKVMMLASSIDNNTFPGGEYFNSSSEKIADVTTTRDWDVNEGLTGGG 300

Query 385 MMTFSQGFHSSNVGMILLQKMGDWTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN 444
MMTFSQGFHSSNVGM LLE+KMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIV+
Sbjct 301 MMTFSQGFHSSNVGMILLQKMGDWTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVS 360

Query 445 IAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS 504
IAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFI+A+YDPNDQT RKSQKEIVGNPVS
Sbjct 361 IAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFITALYDPNDQTVRKSQKEIVGNPVS 420

Query 505 KDAASLRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG 564
KDAAS TRT MVLVGTDVPVYGTMYNHSTGKP VTVPGQNVALKSGTAQIADEKNGGYLVG
Sbjct 421 KDAASQTRTQMVLVGTDVPVYGTMYNHSTGKPIVTVPGQNVALKSGTAQIADEKNGGYLVG 480

Query 565 LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA 624
T+YIFS ++++PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SL LQ+ A
Sbjct 481 STNYIFSLLTINPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLYLQSPA 540

Query 625 KALEQVSQQSPYPMPVSKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQ 684
K L++V+ +S Y MPS+KDISPGDLAEELRRN+VQPIVVGTGTGIK SS EEG+NL+PNQ
Sbjct 541 KNLDKVTTESSYAMPSIKDISPGDLAEELRRNLVQPIVVGTGTGIKESSVEEGRNLSPNQ 600

Query 685 QVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI 744
QVLILSDKAEVPMYGTWKETAET AKWLNIELEF+GSGSTVQKQDVRANTAIKDIKKI
Sbjct 601 QVLILSDKAEVPMYGTWKETAETFAKWLNIIELEFEGSGSTVQKQDVRANTAIKDIKKI 660

Query 745 TLTLGD 750
LTLGD
Sbjct 661 TLTLGD 666

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>emb|CAA67010.1| penicillin-binding protein [Streptococcus pneumoniae]  
Length=666

Score = 1146 bits (2964), Expect = 0.0, Method: Composition-based stats.  
Identities = 586/666 (87%), Positives = 631/666 (94%), Gaps = 0/666 (0%)

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Query 85 VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 144

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Sbjct	1	VPIAEDATSYNVYAVID+ YKSATGKILYVE +QFNKVAEVFHKYLDME+E+YV+EQL+QP VPIAEDATSYNVYAVIDKKYKSATGKILYVEDS QFNKVAEVFHKYLDMEAYVKEQLAQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NL QVSFGAKGNGITYANMM+IKK+L+ A V+GIDFTTSPNRSYPNGQFASSFIGLAQLH NLTQVSFGAKGNGITYANMMAIKKDLK DASVEGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGT G+ESSLN+ILAGTDGIIITYEKD +GNIVPGTE VSQ+T+DGKDVYTT ENEDGSKSLLGTGFGLESSLNTILAGTDGIIITYEKDGVGNIVPGTELVSSQQTVDGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	+SSPLQSFMETQMDAF +KVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVW LSSPLQSFMETQMDAFLQKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFVW	240
Query	325	RDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGR	384
Sbjct	241	RDILYQ NYEPGS MKVM LA++IDNNTFPGGE FNSSE KIAD T RDWDVNEGLTGG RDILYQGNYEPGSAMKVMTLASSIDNNTFPGGEYFNSSSESKIADVTTTRDWDVNEGLTG	300
Query	385	MMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFSQGFHSSNVGM LLE+KMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIV+ MMTFSQGFHSSNVGMILLEKMGDTTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVS	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVG PVS IAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGKPV	420
Query	505	KDAASLRTNMLVVGTDVPYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	+DAASLRTNMLVVGTD+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG EDAASLRTNMLVVGTDPLYGTMYNHQTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGLGEFANPILERASAMKDSLNLQTTA	624
Sbjct	481	T+YIFS V+M+PAENPDFILYVTVQQPEH+SGIGLGEFANPILERASAMK+SLNLQ+ A STNYIFSVVTMNPAENPDFILYVTVQQPEHFSIGLGEFANPILERASAMKESLNLQSPA	540
Query	625	KALEQVSQQSPYPMPVSKDISPGDLAEELRRNLVQPIVVGTTGKIKNSSAEEGKNLAPNQ	684
Sbjct	541	K L+QVS Q+ Y MPS+K+ISPGDLAEELRRN+VQPIVVGTTGKIK SS EEG+NL+PNQ KNLDQVSSQTSYAMPSIKNISPGDLAEELRRNIVQPIVVGTTGKIKESSVEEGRNLSPNQ	600
Query	685	QVLILSDKAAEEVPDMYGWTKETAETLAKWLNIELEFGSGSTVQKQDVRANTAIKDIKKI	744
Sbjct	601	QVLILSDKAAEEVPDMYGWTKETAET AKWLNIELEF+GSGSTVQKQDVRANTAIKDIKKI QVLILSDKAAEEVPDMYGWTKETAETFAKWLNIELEFEGSGSTVQKQDVRANTAIKDIKKI	660
Query	745	TLTLGD 750	
Sbjct	661	+TLGD YITLGD 666	

>gb|AA56856.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=669

Score = 1145 bits (2961), Expect = 0.0, Method: Composition-based stats.  
Identities = 587/669 (87%), Positives = 628/669 (93%), Gaps = 0/669 (0%)

Query	82	RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL	141
Sbjct	1	RNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFNKVAEVFHKYLDME+E+YV+EQL RNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFNKVAEVFHKYLDMEAYVKEQL	60
Query	142	SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLA	201
Sbjct	61	SQPNL QVSFGAKGNGITYANMM+IKKELE AEVKIDFTTSPNRSYPNGQFASSFIGLA SQPNLTQVSFGAKGNGITYANMMAIKKELETAEVKIDFTTSPNRSYPNGQFASSFIGLA	120
Query	202	QLHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDV	261
Sbjct	121	QLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDRLGNIVPGTEQVSQ+T+DGKDV QLHENEDGSKSLLGTSGMESSLNSILAGKDGIIITYEKDRLGNIVPGTEQVSQQTVDGKDV	180
Query	262	YTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITED	321
Sbjct	181	YTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITED YTTLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITED	240
Query	322	FVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLT	381
Sbjct	241	FVWRDILYQSNYEPGS MKVM LA++IDNNTF GE FNSSE KIADAT RDWDVN+GLT FVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPGGEYFNSSSEFKIADATTRDWDVNDGLT	300
Query	382	GGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN	441
Sbjct	301	G MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADN TGGMMTFLQGFHSSNVGMSLLEQKMGDATWLDYLKRKFGVPTRFGLTDEYAGQLPADN	360
Query	442	IVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN	501
Sbjct	361	IV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGN IVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGN	420
Query	502	PVSKDAASLRTNMLVVGTDVPYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGY	561
Sbjct	421	PVSK+AAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGY PVSKEAASLRTNMLVVGTDPLYGTMYNHYTGKPIITVPGQNVAVKSGTAQIADEKNGGY	480

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Query   562  LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ  621
Sbjct   481  LVGSTNYIFSVVTMNPANPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQ  540

Query   622  TTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA  681
Sbjct   541  SPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLA  600

Query   682  PNQQVLILSDKAEVDPMYGWTKETATLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDI  741
Sbjct   601  PNQQVLLSDKVEEIPDMYGWKKETATFAKWLIDIELEFEGSGSVVQKQDVRTNTAIKNI  660

Query   742  KKITLTLGD 750
Sbjct   661  KKI LTLGD
        KKI LTLGD 669

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>gb|AAN32864.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=661

Score = 1143 bits (2956), Expect = 0.0, Method: Composition-based stats.  
Identities = 588/661 (88%), Positives = 625/661 (94%), Gaps = 0/661 (0%)

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Query   90  DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV  149
Sbjct   1  DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV  60

Query   150  SFGAKGNNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG  209
Sbjct   61  SFGAKGNNGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG  120

Query   210  SKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPL  269
Sbjct   121  SKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQ+T+DGKDVTYTTISSPL  180

Query   270  QSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY  329
Sbjct   181  QSFMETQM+AFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEG+T+DFVWRDILY  240

Query   330  QSNYEPGSTMKVMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFS  389
Sbjct   241  QSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN GLT G MMTF  300

Query   390  QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS  449
Sbjct   301  QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSS  360

Query   450  FGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKEAAS  509
Sbjct   361  FGQGISVTQTQMLRAFAATAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAAS  420

Query   510  LTRTNMVLVGTDVPYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNNGGYLVGLTDYI  569
Sbjct   421  TTRNHMILVGTDPLYGTMYNHSTGKPIITVPGQNVAVKSGTAQIADEKNNGGYLVGSTNYI  480

Query   570  FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ  629
Sbjct   481  FSVVTMNPANPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPAKNLDK  540

Query   630  VSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQQVLIL  689
Sbjct   541  VTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGKNLAPNQQVLLL  600

Query   690  SDKAEVDPMYGWTKETATLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLG  749
Sbjct   601  SDK EE+PDYMGW KETAE AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTLG  660

Query   750  D 750
Sbjct   661  D 661

```

>emb|CAA67011.1| penicillin-binding protein [Streptococcus pneumoniae]  
Length=666

Score = 1141 bits (2952), Expect = 0.0, Method: Composition-based stats.  
Identities = 583/666 (87%), Positives = 627/666 (94%), Gaps = 0/666 (0%)

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Query   85  VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP  144
Sbjct   1  VPIAEDATSYNVYAVID+ YKSATGKILYVE +QFNKVAEVFHKYLDME+E+YV+EQL+QP  60

Query   145  NLKQVSFSGAKGNNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH  204
Sbjct   61  NLQVSFSGAKGNNGITYANMM+IKK+L+ A +GIDFTT PNRSYNGQFASSFIGLAQLH  120

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Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGT G+ESSLN+ILAGTDGIIITYEKDR+GNIVPGTE VSQ+T+DGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPFTDADTKEGITEDFVW	324
Sbjct	181	LSSPVQSFMETQMDAFLEKVKGYMTATLVSAKTGEILATTQRPFTFNADTKDGITKDFVW	240
Query	325	RDILYQSNYEPGSTMKVMMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGR	384
Sbjct	241	RDILYQ NYEPGS MKVM LA++IDNNTFPGGE FNSSE KIAD TIRDWDVNEGLTGG	300
Query	385	MMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFSQGFHSSNVG LLE+KMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIV+	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI+A+YDPNDQT RKSQKEIVGNPVS	420
Query	505	KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	KDAAS TRT MVLVGTDPVYGTMYNHSTGKP VTPVQGNVALKSGTAQIADEKNGGYLVG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQLGEFANPILERASAMKDSLNLQTTA	624
Sbjct	481	T+YIFS V+M+PAENPDFILYVTVQQPEH+SGIQLGEFANPILERASAMK+SLNLQ+ A	540
Query	625	KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTTIKNSSAEEGKNLAPNQ	684
Sbjct	541	K L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTTIK +S EEGKNLAPNQ	600
Query	685	QVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVNRANTAIKDIKKI	744
Sbjct	601	QVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI	660
Query	745	TLTLGD 750	
Sbjct	661	LTLGD 666	

>gb|AA56840.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=667

Score = 1140 bits (2949), Expect = 0.0, Method: Composition-based stats.  
Identities = 585/667 (87%), Positives = 626/667 (93%), Gaps = 0/667 (0%)

Query	84	GVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQ	143
Sbjct	1	GVPIAEDATSYNVYAVID+ YKSATGKILYE QFNKVAEVFHKYLDM+E+YV+EQLSQ	60
Query	144	PNLKQVSFGAKNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQL	203
Sbjct	61	PNL QVSFGAKNGGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQL	120
Query	204	HENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	263
Sbjct	121	HENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT	180
Query	264	TISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPFTDADTKEGITEDFV	323
Sbjct	181	T+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPFT+ADTKEGITEDFV	240
Query	324	WRDILYQSNYEPGSTMKVMMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGG	383
Sbjct	241	WRDILYQSNYEPGS MKVM LA++IDNNTFPGGE FNSSE KIADAT RDWDVN+GLT G	300
Query	384	RMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIV	443
Sbjct	301	MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV	360
Query	444	NIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPV	503
Sbjct	361	+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPV	420
Query	504	SKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGGYLV	563
Sbjct	421	SK+AS TR +M+LVGTD+YGTMYNH TGKP +TVPQGNVA+KSGTAQIADEKNGGYLV	480
Query	564	GLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQLGEFANPILERASAMKDSLNLQTT	623
Sbjct	481	G T+YIFS V+M+PAENPDFILYVTVQQPEHYSIGIQLGEFA PILERASAMK+SLNLQ+	540
Query	624	AKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTTIKNSSAEEGKNLAPN	683
Sbjct	541	AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTTIK +S EEG NLAPN	600

```

Query   684   QQVLILSDKAEVPMYGWTKETAETLAKWLNIELEFQGGSGSTVQKQDVRANTAIKDIKK  743
Sbjct   601   QQVLLLSDKVEEIPDMYGWKKETAETFAKWLIDIELEFEGSGSVVQKQDVRTNTAIKNIKK  660

Query   744   ITLTLGD   750
          I   LTLGD
Sbjct   661   IKLTLGD   667

```

>gb|AAN32856.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=661

Score = 1139 bits (2945), Expect = 0.0, Method: Composition-based stats.  
Identities = 586/661 (88%), Positives = 624/661 (94%), Gaps = 0/661 (0%)

```

Query   90   DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV  149
Sbjct   1    DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV  60

Query   150  SFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG  209
Sbjct   61   SFG+KNGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG  120

Query   210  SKSLLGTSGMESSLNSILAGTDGIITYEKDR LGNIVPGTEQVSQRTMDGKDVYTTISSPL  269
Sbjct   121  SKSLLGTSGMESSLNSILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGKDVYTT+SSPL  180

Query   270  QSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY  329
Sbjct   181  QSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILY  240

Query   330  QSNYEPGSTMTKVMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFS  389
Sbjct   241  QSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF  300

Query   390  QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS  449
Sbjct   301  QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSS  360

Query   450  FGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKEAAS  509
Sbjct   361  FGQGISVTQTQMLRAFAATAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAAS  420

Query   510  LTRTNMVLVGTDPVYGYTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGGYLVGLTDYI  569
Sbjct   421  TTRNHMILVGTDPVYGYTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG T+YI  480

Query   570  FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ  629
Sbjct   481  FSVVTMNPANPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPAKNLDK  540

Query   630  VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTTGKTIKNSSAEEGKNLAPNQVLLI  689
Sbjct   541  VTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTTGKTIKETSVEEGTNLAPNQVLLL  600

Query   690  SDKAEVPMYGWTKETAETLAKWLNIELEFQGGSGSTVQKQDVRANTAIKDIKKITLTLG  749
Sbjct   601  SDKVEEIPDMYGWKKETAETFAKWLIDIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTLG  660

Query   750  D   750
          D
Sbjct   661  D   661

```

>gb|ABB46508.1| penicillin binding protein 2x [Streptococcus pneumoniae]  
Length=657

Score = 1135 bits (2936), Expect = 0.0, Method: Composition-based stats.  
Identities = 583/657 (88%), Positives = 620/657 (94%), Gaps = 0/657 (0%)

```

Query   94   YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGA  153
Sbjct   1    YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGA  60

Query   154  KNGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSL  213
Sbjct   61   KNGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSL  120

Query   214  LGTSGMESSLNSILAGTDGIITYEKDR LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSF  273
Sbjct   121  LGTSGMESSLNSILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGKDVYTT+SSPLQSF  180

Query   274  ETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNY  333
Sbjct   181  ETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILYQSNY  240

```



```

Query   334   EPGSTMKVMMMLAAAIIDNNTFPGGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFA 393
Sbjct   241   EPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF QGFA 300
          EPGSAMKVMTLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVDNGLTTGGMMTFLQGFA

Query   394   HSSNVGMTLLEQKMGDATTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG 453
Sbjct   301   HSSNVGM+LLEQKMGDATTWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQG 360
          HSSNVGMSLLEQKMGDATTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQG

Query   454   ISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAASLTRT 513
Sbjct   361   ISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR 420
          ISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRN

Query   514   NMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV 573
Sbjct   421   HMILVGTDPLYGTMYNHYTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVV 480
          +M+LVGTD+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG T+YIFS V

Query   574   SMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQ 633
Sbjct   481   +M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ AK L++V+ + 540
          TMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPAKNLDKVTTE

Query   634   SPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTTGKTIKNSSAEEGKNLAPNQVVLISDKA 693
Sbjct   541   S Y MPS+KDISPG+LAE LRRN+VQPIVVGTTGTKIK +S EEG NLAPNQVVL+LSDK 600
          SSYAMPSIKDISPGELAEALRRNIVQPIVVGTTGTKIKETSVEEGTNLAPNQVVLISDKV

Query   694   EEVPDMYGWTKETATLAKWLNIELEFQSGSGSTVQKQDV RANTAIKDIKKITLTLGD 750
Sbjct   601   EE+PDMYGW KETAT AKWL+IELEF+GSGS VQKQDVR NTAIK+I KI LTLGD 657
          EEIPDMYGWKKETATFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNITKIKLTLGD

```

>gb|AA556855.1| penicillin-binding protein 2X [Streptococcus pneumoniae]  
Length=669

Score = 1135 bits (2935), Expect = 0.0, Method: Composition-based stats.  
Identities = 580/669 (86%), Positives = 626/669 (93%), Gaps = 0/669 (0%)

```

Query   82    RNVVPIAEDATSYNVYVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL 141
Sbjct   1     RNVVPIAEDATSYNVYVID+ YKSATGKILYVE QFNKVAEVFHKYLDME+YV+EQL 60
          RNVVPIAEDATSYNVYVIDKKYKSATGKILYVEDAQFNKVAEVFHKYLDMEAYVKEQL

Query   142   SQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA 201
Sbjct   61    SQPNL QVSFGAKNGITYANMM+IKK+L+ A V+GIDFTTSPNRSYPNGQFASSFIGLA 120
          SQPNLTQVSFGAKNGITYANMMAIKKDLKADASVEGIDFTTSPNRSYPNGQFASSFIGLA

Query   202   QLHENEDGSKSLGTSGLSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV 261
Sbjct   121   QLHENEDGSKSLGTSGLSG+ESSLN+ILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDV 180
          QLHENEDGSKSLGTSGLSGLESSLNTILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDV

Query   262   YTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITED 321
Sbjct   181   YTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITED 240
          YTTLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITED

Query   322   FVWRDILYQSNEYEPGSTMKVMMMLAAAIIDNNTFPGGGEVFNSSSELKIADATIRDWDVNEGLT 381
Sbjct   241   FVWRDILYQSNEYEPGS KVMMLA++IDNNTFP GE FNSSE KIADAT RDWDVN GLT 300
          FVWRDILYQSNEYEPGSAFKVMMMLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNAGLT

Query   382   GGRMMTFSQGFAHSSNVGMTLLEQKMGDATTWLDYLNRFKFGVPTRFGLTDEYAGQLPADN 441
Sbjct   301   G MMTF QGFAHSSNVG +LLEQKMGDATTWLDYL RFKFGVPTRFGLTDEYAGQLPADN 360
          TGGMMTFLQGFAHSSNVGTSLLLEQKMGDATTWLDYLNRFKFGVPTRFGLTDEYAGQLPADN

Query   442   IVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN 501
Sbjct   361   IV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGN 420
          IVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGN

Query   502   PVS KDAASLTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGY 561
Sbjct   421   PVS K+AAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGY 480
          PVSKEAASSTRNHMILVGTDPLYGTMYNHYTGKPIITVPGQNVAVKSGTAQIADEKNGGY

Query   562   LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ 621
Sbjct   481   LVG T+YIFS V+M+PAENPDFILYVTVQQPEH+SGIQLGEFA PILERASAMK+SLNLQ 540
          LVGSTNYIFSVVTMNPAENPDFILYVTVQQPEHFSGIQLGEFATPILERASAMKESLNLQ

Query   622   TTA KALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTTGKTIKNSSAEEGKNLA 681
Sbjct   541   + AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTTGTKIK +S EEG NLA 600
          SPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTTGTKIKETSVEEGTNLA

Query   682   PNQQVVLISDKAAEEVPDMYGWTKETATLAKWLNIELEFQSGSGSTVQKQDV RANTAIKDI 741
Sbjct   601   PNQQVVL+LSDK EE+PDMYGW KETAT AKWL+IELEF+GSGS VQKQDVR NTAIK+I 660
          PNQQVVLISDKVVEEIPDMYGWKKETATFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNI

Query   742   KKITLTLGD 750
Sbjct   661   KKI LTLGD 669
          KKI LTLGD
          KKIKLTLGD

```



Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects  
Posted date: May 31, 2007 5:55 PM  
Number of letters in database: 146,036  
Number of sequences in database: 262

Lambda	K	H
0.313	0.130	0.362

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of Sequences: 262  
Number of Hits to DB: 1868  
Number of extensions: 66  
Number of successful extensions: 3  
Number of sequences better than 10: 1  
Number of HSP's better than 10 without gapping: 0  
Number of HSP's gapped: 1  
Number of HSP's successfully gapped: 1  
Length of query: 750  
Length of database: 146036  
Length adjustment: 77  
Effective length of query: 673  
Effective length of database: 125862  
Effective search space: 84705126  
Effective search space used: 84705126  
T: 11  
A: 40  
X1: 16 (7.2 bits)  
X2: 38 (14.6 bits)  
X3: 64 (24.7 bits)  
S1: 42 (20.8 bits)  
S2: 48 (23.1 bits)